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(54) Title: PROLYL PEPTIDASES AND METHODS OF USE (57) Abstract The present invention provides isolated polypeptides, prolyl tripeptidyl-peptidases, and active analogs, active fragments or active modifications thereof, having amidolytic activity for cleavage of a peptide bond present in a target peptide having at least 30 amino acids. Isolated nucleic acid fragments encoding isolated prolyl tripeptidyl-peptidases are also provided, as are methods of reducing growth of a bacterium by inhibiting a prolyl tripeptidyl-peptidase.		

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PROLYL PEPTIDASES AND METHODS OF USE

CONTINUING APPLICATION DATA

This patent application claims the benefit of U.S. provisional patent application No. 60/123,148, filed March 5, 1999, which is incorporated by reference herein.

GOVERNMENT FUNDING

The present invention was made with government support under Grant No. DE 09761, awarded by the National Institutes of Health. The Government may have certain rights in this invention.

BACKGROUND OF THE INVENTION

Porphyromonas gingivalis (formerly *Bacteroides gingivalis*) is an obligately anaerobic bacterium which is implicated in periodontal disease. *P. gingivalis* produces several distinct proteolytic enzymes, many of which are recognized as important virulence factors. A number of physiologically significant proteins, including collagen, fibronectin, immunoglobulins, complement factors C3, C4, C5, and B, lysozyme, iron-binding proteins, plasma proteinase inhibitors, fibrin and fibrinogen, and factors of the plasma coagulation cascade system, are hydrolyzed by *P. gingivalis* proteases. Broad proteolytic activity plays a role in the evasion of host defense mechanisms and the destruction of gingival connective tissue in progressive periodontitis.

Progressive periodontitis is characterized by acute tissue degradation promoted by collagen digestion and a vigorous inflammatory response characterized by excessive neutrophil infiltration. Gingival crevicular fluid accumulates in periodontitis as periodontal tissue erosion progresses at the foci of the infection, and numerous plasma proteins are exposed to proteinases expressed by the bacteria at the injury site. Neutrophils are recruited to the gingiva, in part, by the humoral chemotactic factor C5a. The complement components C3 and C5 are activated by complex plasma proteases with "trypsin-like" specificities called convertases. The human plasma convertases

cleave the α -chains of C3 and C5 at a specific site generating biologically active factors known as anaphylatoxins (i.e. C3a and C5a). The anaphylatoxins are potent proinflammatory factors exhibiting chemotactic and/or spasmogenic activities as well as promoting increased vascular permeability. The larger products from C3 and C5 cleavage (i.e. C3b and C5b) participate in functions including complement cascade activation, opsonization, and lytic complex formation.

Recent studies have indicated that this periodontopathogen produces at least seven different enzymes belonging to the cysteine and serine catalytic classes of peptidases, among which three cysteine proteinases (gingipains) are predominant (Potempa, J., et al. (1995) *Prospect. Drug Discovery and Design* 2, 445-458). The gingipains are the best characterized group of *P. gingivalis* enzymes as their structure, function, enzymatic properties and pathological significance are known. From *in vitro* studies it is apparent that two gingipains R (also referred to generally as "Arg-gingipains" and more specifically as RgpA and RgpB), enzymes specific for cleavage at Arg-Xaa peptide bonds, have a significant potential to contribute to the development and/or maintenance of a pathological inflammatory state in infected periodontal pockets through: (i) activation of the kallikrein-kinin cascade, (ii) the release of neutrophil chemotactic activity from native and oxidized C5 of the complement pathway, and (iii) activation of factor X. In addition, gingipain K (also referred to as "Lys-gingipain"), an enzyme which cleaves Lys-Xaa peptide bonds, degrades fibrinogen. This may add to a bleeding on probing tendency associated with periodontitis. Finally, the presence of a hemagglutinin/adhesion domain in the non covalent multiprotein complexes of RgpA and gingipain K suggests participation of these enzymes in the binding of *P. gingivalis* to extracellular matrix proteins which may facilitate tissue invasion by this pathogen.

In comparison to the gingipains, relatively little is known about other cysteine proteinases produced by *P. gingivalis*. Two genes, referred to as *tp*r and *p*rtT have been cloned and sequenced and although they encode a putative papain-like and streptopain-like cysteine proteinases, respectively, neither has been purified and characterized.

The presence of serine proteinase activity in cultures of *P. gingivalis* has been known for several years; however, only limited information is available about such enzymes. Indeed, a serine endopeptidase has been isolated from culture media, although it was only superficially characterized (Hinode D., et al.,
5 (1993) *Infect. Immun.* 59, 3060-3068). On the other hand, an enzyme referred to as glycylprolyl peptidase (DPP IV) was found to be associated with bacterial surfaces and two molecular mass forms of this peptidase have been described. This enzyme has also been shown to possess the ability to hydrolyze partially degraded type I collagen, releasing the Gly-Pro dipeptide, and it was suggested
10 that, in collaboration with collagenase, glycylprolyl peptidase may contribute to the destruction of the periodontal ligament (Abiko, Y., et al. (1985) *J.Dent. Res.* 64, 106-111). In addition to this potential pathological function, glycylprolyl peptidase may also play a vital role in providing *P. gingivalis* with dipeptides which can be transported inside the cell and serve as a source of carbon,
15 nitrogen, and energy for this asaccharolytic organism. Recently, a gene encoding glycylprolyl peptidase in *P. gingivalis* has been cloned and sequenced, and it is now apparent that this enzyme is homologous to dipeptidyl-peptidase IV (DPP-IV) from other organisms (Kiyama, M., et al. (1998) 1396, 39-46). The nucleotide sequence of the genome of this bacterium is currently being
20 determined by The Institute for Genomic Research, and is available at www.tigr.org.

SUMMARY OF THE INVENTION

The present invention is directed to an isolated prolyl tripeptidyl-
25 peptidase, active analog, active fragment, or active modification thereof having amidolytic activity for cleavage of a peptide bond present in a target polypeptide having at least 4 amino acids. Alternatively, the isolated prolyl tripeptidyl-peptidase, active analog, active fragment, or active modification thereof is isolated from *P. gingivalis*. Typically, amidolytic activity is determined with a
30 prolyl tripeptidyl-peptidase:target polypeptide ratio of at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours. The peptide cleaved by the isolated prolyl tripeptidyl-peptidase can include the sequence of SEQ ID NO:1, SEQ ID NO:2, SEQ ID

NO:7, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:11, H-Ala-Arg-Pro-Ala-D-Lys-amide, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:25, or SEQ ID NO:37. The amino acid sequence of the isolated prolyl tripeptidyl-peptidase can include the amino acid sequence GXSTXXG (SEQ ID NO:39), the amino acid sequence GXSTXGG (SEQ ID NO:40), or the amino acid sequence of SEQ ID NO:30.

Another aspect of the invention is an isolated polypeptide, active analog, active fragment, or active modification thereof having amidolytic activity for cleavage of a peptide bond present in a target polypeptide having at least 4 amino acids. Typically, the polypeptide:target polypeptide ratio of at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours.

The invention is also directed to an isolated polypeptide comprising an amino acid sequence having a percentage amino acid identity of greater than 35 % with SEQ ID NO:30.

An alternative aspect of the invention is an isolated nucleic acid fragment encoding a prolyl-tripeptidyl peptidase, active analog, active fragment, or active modification thereof, having amidolytic activity for cleavage of a peptide bond present in a target polypeptide having at least 4 amino acids. Typically, the prolyl tripeptidyl-peptidase:target polypeptide ratio of at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours. The nucleic acid fragment can have a nucleotide sequence comprising SEQ ID NO:38. A complement of the nucleic acid fragment can hybridize to SEQ ID NO:38 under hybridization conditions of 0.5 M phosphate buffer, pH 7.2, 7 % SDS, 10 mM EDTA, at 68°C, followed by three for 20 minutes washes in 2x SSC, and 0.1 % SDS, at 65°C, wherein at least about 20 nucleotides of the complement hybridize.

Another aspect of the invention is an isolated nucleic acid fragment encoding a polypeptide that includes an amino acid sequence having a percentage amino acid identity of greater than 35 % with SEQ ID NO:30.

The invention is also directed at a method of identifying an inhibitor of a prolyl-tripeptidyl peptidase, active analog, active fragment, or active modification thereof, including identifying a molecule that inhibits the

amidolytic activity of the prolyl-tripeptidyl peptidase. The inhibitor is identified by incubating the prolyl-tripeptidyl peptidase with the molecule under conditions that promote amidolytic activity of the prolyl-tripeptidyl peptidase and determining if the amidolytic activity of the prolyl-tripeptidyl peptidase is inhibited relative to the amidolytic activity in the absence of molecule.

An aspect of the invention is a method of reducing growth of a bacterium. This method includes inhibiting a prolyl tripeptidyl-peptidase, active analog, active fragment, or active modification thereof, or a prolyl dipeptidyl-peptidase, active analog, active fragment, or active modification thereof. The method includes contacting the prolyl tripeptidyl-peptidase with an inhibitor of the prolyl tripeptidyl-peptidase. The method can be used to protect an animal from a periodontal disease caused by *P. gingivalis* including administering to the animal the inhibitor. The disease can be selected from the group consisting of gingivitis and periodontitis. The inhibitor can be administered by a method selected from the group consisting of subgingival application and controlled release delivery.

Another aspect of the invention is an immunogenic composition including an isolated prolyl tripeptidyl-peptidase, or an antigenic analog, antigenic fragment, or antigenic modification thereof, the prolyl tripeptidyl-peptidase having amidolytic activity for cleavage of a peptide bond present in a target peptide having at least 4 amino acids. Typically, the prolyl tripeptidyl-peptidase:target polypeptide ratio is at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours. The immunogenic composition can include an adjuvant.

The invention is also directed to a composition including an inhibitor of an isolated prolyl tripeptidyl-peptidase and a pharmaceutically acceptable carrier.

Additional aspects of the invention include a dipeptidyl peptidase having an amino acid sequence including SEQ ID NO:43, SEQ ID NO:44, or SEQ ID NO:45.

Definitions

“Polypeptide” as used herein refers to a polymer of amino acids and does not refer to a specific length of a polymer of amino acids. Thus, for example, the terms peptide, oligopeptide, protein, and enzyme are included within the definition of polypeptide. This term also includes post-expression modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations, and the like. A polypeptide can be produced by an organism, or produced using recombinant techniques, or chemically or enzymatically synthesized.

“Peptidase,” “proteinase,” and “protease” all refer to enzymes that catalyze the hydrolysis of peptide bonds in a polypeptide. A “peptide bond” or “amide bond” is a covalent bond between the alpha-amino group of one amino acid and the alpha-carboxyl group of another amino acid. “Peptidase inhibitor,” “proteinase inhibitor,” “protease inhibitor,” and “inhibitor” all refer to molecules that inhibit a peptidase that catalyzes the hydrolysis of peptide bonds in a polypeptide.

As used herein, the term “isolated” means that a polypeptide or a nucleic acid fragment has been either removed from its natural environment, produced using recombinant techniques, or chemically or enzymatically synthesized. Preferably, the polypeptide or nucleic acid fragment is purified, i.e., essentially free from any other polypeptides or nucleic acid fragments and associated cellular products or other impurities.

“Amidolytic activity” refers to the ability of a polypeptide to catalyze the hydrolysis of at least one peptide bond in a polypeptide. The term “cleavage” can also be used to refer to the hydrolysis of a peptide bond in a polypeptide. “Prolyl-tripeptidyl peptidase” and “PTP” refer to a polypeptide having a particular “amidolytic activity”. A “prolyl-tripeptidyl peptidase” is able to hydrolyze the peptide bond between the proline and the Yaa residues in a target polypeptide with the general formula $\text{NH}_2\text{-Xaa-Xaa-Pro-Yaa-(Xaa)}_n$ (SEQ ID NO:25), wherein Xaa is a natural or modified amino acid, Yaa is a natural or modified amino acid except proline, and the α -amino of the amino terminal residue is not blocked. A “prolyl tripeptidyl-peptidase” does not have to cleave all members of the target peptide. The term “natural amino acid” refers to the 20 amino acids typically produced by a cell. The term “modified amino acid”

refers to, for instance, acetylation, hydroxylation, methylation, amidation, and the attachment of carbohydrate or lipid moieties, cofactors, and the like.

A "target polypeptide" is a polypeptide that is the potential substrate of the amidolytic activity of a prolyl tripeptidyl-peptidase.

5 An active analog, active fragment, or active modification of a polypeptide of the invention is one that has amidolytic activity by hydrolysis of a peptide bond present in the target polypeptide as described herein. Active analogs, fragments, and modifications are described in greater detail herein.

10 "Nucleic acid fragment" as used herein refers to a linear polymeric form of nucleotides of any length, either ribonucleotides or deoxynucleotides, and includes both double- and single-stranded DNA and RNA. A nucleic acid fragment may include both coding and non-coding regions that can be obtained directly from a natural source (e.g., a microorganism), or can be prepared with the aid of recombinant or synthetic techniques. A nucleic acid molecule may be
15 equivalent to this nucleic acid fragment or it can include this fragment in addition to one or more other nucleotides or polynucleotides. For example, the nucleic acid molecule of the invention can be a vector, such as an expression of cloning vector.

20 "Percentage amino acid identity" refers to a comparison of the amino acids of two polypeptides as described herein.

BRIEF DESCRIPTION OF THE FIGURES

25 **Fig. 1. Purification of the prolyl tripeptidyl peptidase from the acetone precipitate of the *P. gingivalis* cell extracts. Absorbance at 280 nm (open triangles), amidolytic activity against H-Ala-Phe-Pro-pNA (closed diamonds), and H-Gly-Pro-pNA (closed circles). (a) Separation of PTP-A on hydroxyapatite. (b) Separation of PTP-A on Phenyl-Sepharose HP. (c) Separation of PTP-A on MonoQ FPLC. (d) Chromatofocusing of PTP-A on Mono-P.**

30 **Fig. 2. SDS -PAGE of fractions from purification of PTP-A and the autoradiography of the purified enzyme. Lane a, molecular mass markers (phosphorylase B, 97 kDa; bovine serum albumin, 68 kDa; ovalbumin, 43 kDa; carbonic anhydrase, 30 kDa; soybean trypsin inhibitor, 20 kDa; α -lactalbumin, 14**

kDa); *lane b*, acetone precipitate from Triton X-100 extract of *P. gingivalis*, *lane c*: hydroxyapatite column eluate; *lane d*, Phenyl-Sepharose column eluate; *lane e*, MonoQ column eluate; *lane f*, purified PTP-A from MonoP column wash; *lane g*, autoradiograph of ^3H -DFP labeled enzyme exposed for 96 h to X-ray film. All samples were reduced and boiled prior to PAGE analysis.

Fig. 3. Multiple sequence alignment of *P. gingivalis* PTP-A (PTP-A) and its bacterial and eukaryotic homologues. Pg-DPP, DPP from *P. gingivalis* (Kiyama, M., et al., (1998) *Bioch. Bioph. Acta* **1396**, 39-46) containing an amino-terminal sequence corrected according to the *P. gingivalis* W83 genome data available from The Institute of Genomic Research at www.tigr.org); Fm-DPP, DPP from *Flavobacterium meningosepticum*; Hs-DPP, human DPP IV; and Mm-FAP, mouse fibroblast activation protein. Peptide sequences obtained from PTP-A analysis described herein are indicated with arrows (note that the sequence of the peptide 81-97 corresponds to the N-terminus of the lower molecular weight form of PTP-A); catalytic triad is marked with asterisks; and the proposed PTP-A membrane-anchoring N-terminal α -helix is double-underlined. Homologous regions (i.e., regions of identical amino acids and/or conservative substitutions) are highlighted. Identical regions are shown as white letters on a black background.

Fig. 4. Comparison of *P. gingivalis* PTP-A and DPP active site domains to corresponding sequences of three putative homologues identified within the *P. gingivalis* genome (DPP-H1, DPP-H2 and DPP-H3). Sequences of *P. gingivalis* PTP-A, DPP, DPP-H1, DPP-H2, and DPP-H3 were obtained from conceptual translation of the following open reading frames retrieved from The Institute for Genomic Research (TIGR) unfinished *P. gingivalis* genome database: gnl | TIGR | *P. gingivalis* contig 126 (positions 13 228 – 15 426), contig 87 (positions 6 424 – 4 399), contig 65 (positions 161 – 1 786), contig 101 (positions 8 895 – 6 845), and contig 9 (positions 4 216 – 2 162), respectively. Residues predicted as catalytic triads are marked with asterisks. Homologous regions (i.e., regions of identical amino acids and/or conservative substitutions) are highlighted.

Identical regions are shown as white letters on a black background. Similar regions (i.e., conservative substitutions) are shown as white letters on a grey background.

5 **Fig. 5. Influence of Pefabloc-serine proteinase inhibitor on *P. gingivalis* growth.**

Fig. 6. Comparison of *P. gingivalis* PTP-A and DPP to sequences of three putative homologues identified within the *P. gingivalis* genome (DPP-H1, DPP-H2 and DPP-H3). Sequences of *P. gingivalis* PTP-A (126PP), DPP (87PP),
10 DPP-H1 (65PP), DPP-H2 (101PP), and DPP-H3 (9PP) were obtained as described in Fig. 4. Homologous regions (i.e., regions of identical amino acids and/or conservative substitutions) are highlighted. Identical regions are shown as white letters on a black background. Similar regions (i.e., conservative substitutions) are shown as white letters on a grey background.

15 **Fig. 7. Nucleotide sequence (SEQ ID NO:38) and amino acid sequence (SEQ ID NO:30) of PTP-A.**

DETAILED DESCRIPTION OF THE INVENTION

20 The present invention provides isolated polypeptides, preferably isolated prolyl peptidases, more preferably prolyl dipeptidyl-peptidases and prolyl tripeptidyl-peptidases, most preferably prolyl-tripeptidyl peptidases, that have amidolytic activity by hydrolysis of a peptide bond present in a target polypeptide, where the bond is between a proline and an amino acid residue attached to the
25 alpha-carboxyl group end of the proline.

When the prolyl peptidase is a prolyl tripeptidyl-peptidase, the peptidase has amidolytic activity by hydrolysis of a peptide bond present in a target polypeptide of the general formula $\text{NH}_2\text{-Xaa-Xaa-Pro-Yaa-(Xaa)}_n$ (SEQ ID NO:25), wherein Xaa is a natural or modified amino acid, Yaa is a natural or
30 modified amino acid except proline, and the α -amino of the amino terminal residue is not blocked, wherein the peptide bond of the target polypeptide that is hydrolyzed is the Pro-Yaa peptide bond. Preferably, isolated polypeptides do not cleave a target peptide having a blocked α -amino of the amino terminal residue.

Preferably, the only peptide bond of the target peptide that is hydrolyzed is the Pro-Yaa bond. In increasing order of preference, isolated polypeptides can cleave a target peptide that is at least 4 amino acids or at least 300 Da, at least 10 amino acids or at least 750 Da, at least 20 amino acids or at least 1,500 Da, or at least 30 amino acids or at least 3,000 Da. Preferably, the prolyl-tripeptidyl peptidases cleave peptides 1, 2, 7, 8, and 10-15 shown in Table 3, human cystatin C, and interleukin 6.

When the prolyl peptidase is a prolyl dipeptidyl-peptidase, the peptidase has amidolytic activity by hydrolysis of a peptide bond present in a target polypeptide of the general formula $\text{NH}_2\text{-Xaa-Zaa-Yaa-(Xaa)}_n$ (SEQ ID NO:12), wherein Xaa is a natural or modified amino acid, Zaa is a proline or alanine, Yaa is a natural or modified amino acid except proline or hydroxyproline, and the α -amino of the amino terminal residue is not blocked, wherein the peptide bond of the target polypeptide that is hydrolyzed is the Zaa-Yaa peptide bond. Preferably, isolated polypeptides does not cleave a target peptide having a blocked α -amino of the amino terminal residue. Preferably, the only peptide bond of the target peptide that is hydrolyzed is the Pro-Yaa bond.

Due to their cyclic aliphatic character proline residues bestow unique conformational constraints on polypeptide chain structures, significantly affecting the susceptibility of proximal peptide bonds to proteolytic cleavage. Those proline residues, which often appear near the amino-termini of many biologically active peptides, may protect them against proteolytic degradation by peptidases with general specificity. A specialized group of proteolytic enzymes, typically referred to as prolyl peptidases, has evolved to cleave (i.e., hydrolyze) a peptide bond adjacent to a proline residue in a polypeptide. The peptide bond adjacent to a proline residue can be referred to as a prolyl-X bond, where prolyl is the proline residue, and X is an amino acid residue attached to the alpha-carboxyl group end of the proline. The bacterial prolyl peptidases can cleave a polypeptide to liberate a tripeptide or a dipeptide. Prolyl peptidases that do not cleave a target peptide if the α -amino of the amino terminal residue is blocked can be referred to as exopeptidases. The *in vivo* activity of these specialized proteolytic enzymes may have important physiological significance, because it may lead to inactivation of many biologically active peptides and/or transformation of the activity of other

biologically active peptides. In addition, hydrolysis of prolyl-X bonds in conjunction with general catabolic pathways should allow the complete re-utilization of amino acids by living organisms, including bacteria. However, prolyl peptidases from bacterial pathogens, if released into the host environment, may interfere with the physiological functions of biologically active polypeptides and, therefore, contribute to the pathogenicity of infectious disease.

The external (i.e., cell surface) localization and uncontrolled activity of bacterial peptidases, including prolyl peptidases, likely contributes significantly to run-away inflammation in the human host and the pathological degradation of connective tissue during periodontitis. For instance, working in concert bacterial prolyl peptidases (e.g., prolyl tripeptidyl peptidases and DPP IV) have the ability to completely degrade collagen fragments locally generated by endogenous or bacterial collagenases. Because type I collagen is the major component of periodontal ligament, its enhanced degradation by bacterial prolyl peptidases may contribute to loss of tooth attachment and periodontal pocket formation. Thus, there is a need in the art to characterize bacterial peptidases to facilitate the development of therapies to inhibit the activity of the bacterial peptidases.

The polypeptides of the present invention, preferably prolyl peptidases, can be used as a source of antibodies for inhibiting the peptidase activity and thereby possibly reducing periodontitis, loss of tooth attachment and periodontal pocket formation. Antibodies to prolyl peptidases can also be used to identify and/or isolate additional prolyl peptidases. Knowledge of prolyl peptidases can also be used to make inhibitors of prolyl peptidases and to make immunogenic compositions that could be used to elicit the production of antibodies to prolyl peptidases and thereby possibly reduce gingivitis, periodontitis, loss of tooth attachment, and/or periodontal pocket formation.

An example of a prolyl-tripeptidyl peptidase is prolyl-tripeptidyl peptidase A (SEQ ID NO:30) (also referred to as PTP-A) from *P. gingivalis*. Purified PTP-A has apparent molecular masses of 81.8 and 75.8 kDa. The lower molecular mass peptidase may be due to the proteolytic cleavage of the peptidase from the surface of *P. gingivalis*. PTP-A is a new member of clan SC, family S9 of serine peptidases. Clans of serine peptidases are grouped on the basis of the order of certain amino acids in the polypeptide that make up the "catalytic triad" which

plays a pivotal role peptidase activity. The members of the clan SC are characterized by the catalytic triad in the polypeptide in the order of serine, aspartic acid, and histidine. Members of the clan SC are also characterized by a tertiary structure including $\beta/\alpha/\beta$ units, and an α/β hydrolase fold. In addition to the catalytic triad order, the amino acid sequence GXSEXG (SEQ ID NO:39), where X is any amino acid and S is the active site serine, is a signature of all members of the clan SC with some distinguishing features specific for each family. Family S9 has the consensus sequence GXSEXG (SEQ ID NO:40). Besides this consensus sequence, there is a general similarity of primary structures which classifies peptidases to this family. For instance, peptidases of this family generally have two domains, an amino-terminal domain that contains a membrane binding domain, and a carboxy-terminal domain, also referred to as the catalytic domain. The catalytic domain contains the residues of the catalytic triad. Some members of the S9 family have only the catalytic domain.

The S9 family is diverged and divided in three subfamilies: S9A, cytosolic oligopeptidases from archae and eukaryotes; S9B, eukaryotic acylaminoacylpeptidases; and S9C, dipeptidyl peptidase IV from bacteria and eukaryotes. The catalytic domain of peptidases from family S9 typically begin at about residue 400 of SEQ ID NO:30 and include the remaining carboxy-terminal amino acids (see, e.g., Fulop, et al., (1998) *Cell* 94, 161-170). Despite structural similarities to peptidases from the S9 family, the tripeptidyl-peptidase activity of PTP-A is unusual for this family of enzymes, and no other known similar activity has so far been attributed to any other member of the S9 family. In fact, all strict tripeptidyl-peptidases belong only to the subtilisin family (S8) and S33 family of serine peptidases; however, they neither share a structural relationship with PTP-A nor have activity limited to cleavage after proline residues. In particular, there are no other known prolyl tripeptidyl peptidases with an activity that is increased by iodoacetamide relative to the same prolyl tripeptidyl peptidase in the absence of iodoacetamide under the same conditions. Iodoacetamide is a compound that is traditionally a peptidase inhibitor. Typically, the activity of a prolyl tripeptidyl peptidase is increased about two-fold. Furthermore, unlike oligopeptidases, the prolyl tripeptidyl-peptidases of the present invention can cleave target peptidases having as few as 4 amino acids but also target peptides having at least 30 amino

acids or a molecular weight of at least 3,000 Da. In these respects, the *P. gingivalis* tripeptidyl peptidase is a unique enzyme, and the isolation and characterization of this novel bacterial prolyl peptidase will facilitate the development of therapies to inhibit the activity of the bacterial peptidases.

5 Examples of putative prolyl-dipeptidyl peptidases are DPP-H1 (SEQ ID NO:43), DPP-H2 (SEQ ID NO:44), and DPP-H3 (SEQ ID NO:45). These peptidases have a significant percentage amino acid similarity with DPP IV and PTP-A (see Fig. 6). Each dipeptidyl peptidase is expected to have enzymatic activity, as each has a well preserved catalytic triad (Fig. 4). DPP IV has been
10 characterized and the gene encoding the peptidase has been cloned, however the substrate specificity has not been well characterized. DPP IV has been found to cleave SEQ ID NOs:6, 20, 23, and 24. DPP IV has been purified in two forms. One of the forms is a full length gene translation product containing a blocked amino-terminal residue. The second form had the amino-terminal amino acid
15 sequence HSYRAAVYDYDVRRLVKPLSEHVG (SEQ ID NO:48), which corresponds to residues 116-140 of DPP IV (Kiyama, M., et al. (1998) 1396, 39-46), indicating that it was proteolytically truncated on the amino-terminus.

 In *P. gingivalis*, PTP-A and DPP IV activity is cell surface associated. While not intending to be limiting, it is conceivable that the enzyme is membrane
20 anchored through a putative signal sequence which is not cleaved but remains as a membrane spanning domain similar to other members of the prolyl oligopeptidase family. However, a significant portion of the purified PTP-A has a truncated N-terminus, apparently due to cleavage by Lys-specific peptidase and likely to be an artifact which has occurred during the purification procedure. Nevertheless,
25 membrane bound PTP-A and DPP IV is proteolytically cleaved and shed during cultivation of the bacteria, as indicated by variable amount of soluble activities found in cell free culture media. The cell surface localization of PTP-A supports a putative physiological function in providing nutrients for growing bacterial cells. The inability of asaccharolytic *P. gingivalis* to utilize free amino acids makes the
30 bacterium entirely dependant on an external peptide supply. In this regard, PTP-A and DPP IV activities are probably very important, if not indispensable, for bacterial growth, and inhibition of prolyl tripeptidyl-peptidases and dipeptidyl-peptidases may inhibit the *in vivo* growth of organisms, including *P. gingivalis*.

For instance, treatment of *P. gingivalis* cultures in lagphase (i.e., the period after inoculation of a culture and before the organism begins to divide) and early logarithmic growth with the inhibitors PEFABLOCK and 3,4-dichloroisocoumarin inhibits growth of *P. gingivalis*.

5 Preferably, a polypeptide of the invention, preferably a prolyl peptidase, contains the amino acid sequence GXSTXG (SEQ ID NO:39), most preferably, GXSTGG (SEQ ID NO:40), where G is glycine, X is any amino acid, and S is the active site serine. The active site serine can be identified by, for instance, labeling with diisopropylfluorophosphate as described herein. Preferably, the catalytic
10 domain of the prolyl tripeptidyl-peptidases of the invention begins at about residue 400 of SEQ ID NO:30 and includes the remaining carboxy-terminal amino acids and the corresponding amino acids of SEQ ID NOs:43-45 (see Fig. 6), more preferably, at about residue 502 of SEQ ID NO:30 and includes the remaining carboxy-terminal amino acids and the corresponding amino acids of SEQ ID
15 NOs:43-45 (see Fig. 6), most preferably, at about residue 556 of SEQ ID NO:30 and includes the remaining carboxy-terminal amino acids and the corresponding amino acids of SEQ ID NOs:43-45 (see Fig. 6).

 The invention further includes a polypeptide, preferably a prolyl tripeptidyl-peptidase, that shares a significant level of primary structure with SEQ ID NO:30.
20 The two amino acid sequences (i.e., the amino acid sequence of the polypeptide and the sequence SEQ ID NO:30) are aligned such that the residues that make up the catalytic triad, i.e., the serine, aspartic acid, and the histidine, are in register, then further aligned to maximize the number of amino acids that they have in common along the lengths of their sequences; gaps in either or both sequences are permitted
25 in making the alignment in order to place the residues of the catalytic triad in register and to maximize the number of shared amino acids, although the amino acids in each sequence must nonetheless remain in their proper order. The percentage amino acid identity is the higher of the following two numbers: (a) the number of amino acids that the two sequences have in common within the
30 alignment, divided by the number of amino acids in SEQ ID NO:30, multiplied by 100; or (b) the number of amino acids that the two sequences have in common within the alignment, divided by the number of amino acids in the candidate polypeptide, multiplied by 100. Preferably, a prolyl tripeptidyl peptidase has

greater than 35 % identity, more preferably at least about 40 % identity, most preferably at least about 45 % identity with SEQ ID NO:30. Preferably, amino acids 154-732 of SEQ ID NO:30 are used, more preferably amino acids 400-732 of SEQ ID NO:30 are used. An isolated polypeptide comprising an amino acid
5 sequence having a percentage amino acid identity of greater than 35 % with SEQ ID NO:30.

In general, the amidolytic activity of the polypeptides of the invention, preferably prolyl peptidases, can be measured by assay of the cleavage of a target polypeptide in the presence of prolyl peptidase and a buffer. Preferably, the lower
10 ratio of prolyl tripeptidyl-peptidase to target polypeptide is at least about 1:1, more preferably at least about 1:100, even more preferably at least about 1:1,000, most preferably at least about 1:10,000. Preferably, the higher ratio of prolyl peptidase to target polypeptide is no greater than about 1:10,000,000, more preferably no greater than about 1:1,000,000 and most preferably no greater than about
15 1:100,000. Buffers in which a prolyl peptidase is active are suitable for the assay. Preferably, the buffer is about 200 mM HEPES (N-2-hydroxyethylpiperazine,N'-2-ethansulfonic acid), more preferably about 50 mM HEPES, most preferably about 20 mM HEPES. Preferably, the pH of the buffer is at least about pH 6.0 and no greater than pH 8.0, more preferably about pH 7.5. Preferably, the temperature of
20 the assay is at about 37°C. The assay can be carried out for at least about 1 minute to no greater than 24 hours. Preferably, the amidolytic activity of the prolyl peptidases are measured at a prolyl peptidase:target polypeptide ratio of at least about 1:100 to no greater than 1:1,000,000 in about 200 mM HEPES, about pH 7.5 at about 37°C for at least about 3 hours. In general, the time of the assay can vary
25 depending on the substrate and enzyme:substrate ratio. Typically, target peptides are stable under these conditions, and typically it is difficult to detect background levels of hydrolysis in the absence of a prolyl peptidase. Preferably, the assay is allowed to continue until at least 1 % of the target peptide is hydrolyzed.

Prolyl-tripeptidyl peptidases of the present invention preferably are
30 inhibited by a compound chosen from the group consisting of PEFABLOCK (4-(2-aminoethyl)-benzenesulfonyl-fluoride hydrochloride), diisopropylfluorophosphate, and 3,4-dichloroisocoumarin, more preferably PEFABLOCK and diisopropylfluorophosphate, and most preferably diisopropylfluorophosphate. The

peptidases of the present invention are preferably not inhibited by a compound chosen from the group consisting of leupeptin, antipain, E-64, pepstatin, α_1 -proteinase inhibitor, α_1 -antichymotrypsin and α_2 -macroglobulin, most preferably. Significantly and unexpectedly, the amidolytic activity of a prolyl-tripeptidyl
5 peptidase of the present invention is increased by iodoacetamide relative to the prolyl-tripeptidyl peptidase in the absence of iodoacetamide under the same conditions. Preferably, the effect of iodoacetamide on amidolytic activity is measured by incubating in 200 mM HEPES, pH 7.6, at least about 0.1 nM of the prolyl tripeptidyl-peptidase with the inhibitor for about 15 minutes, adding about 1
10 mM of H-Ala-Phe-Pro-pHA, and incubating for at least about 1 minute before assaying for amidolytic activity. Typically, at least about 1 mM to no greater than 100 mM of inhibitor is used.

The polypeptides of the invention include a polypeptide having SEQ ID NO:30, or an active analog, active fragment, or active modification of SEQ ID
15 NO:30. An active analog, active fragment, or active modification of a polypeptide having SEQ ID NO:30 is one that has amidolytic activity by hydrolysis of the Pro-Yaa peptide bond present in a target polypeptide of the general formula $\text{NH}_2\text{-Xaa-Xaa-Pro-Yaa-(Xaa)}_n$ (SEQ ID NO:25). Active analogs of a polypeptide having SEQ ID NO:30 include prolyl-tripeptidyl peptidases having amino acid
20 substitutions that do not eliminate hydrolysis of SEQ ID NO:25 at the Pro-Yaa peptide bond. Substitutes for an amino acid may be selected from other members of the class to which the amino acid belongs. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and tyrosine. Polar neutral amino acids include glycine, serine,
25 threonine, cysteine, tyrosine, asparagine and glutamine. The positively charged (basic) amino acids include arginine, lysine and histidine. The negatively charged (acidic) amino acids include aspartic acid and glutamic acid. Examples of preferred conservative substitutions include Lys for Arg and *vice versa* to maintain a positive charge; Glu for Asp and *vice versa* to maintain a negative charge; Ser for
30 Thr so that a free -OH is maintained; and Gln for Asn to maintain a free NH_2 .

Active fragments of a prolyl-tripeptidyl peptidase of the invention include prolyl-tripeptidyl peptidases containing deletions or additions of one or more contiguous or noncontiguous amino acids such that the resulting polypeptide will

hydrolyze SEQ ID NO:25 at the Pro-Yaa peptide bond. An example of a fragment of a prolyl-tripeptidyl peptidase is a catalytic domain. Modified prolyl-tripeptidyl peptidases include prolyl-tripeptidyl peptidases that are chemically and enzymatically derivatized at one or more constituent amino acid, including side chain modifications, backbone modifications, and N- and C- terminal modifications including acetylation, hydroxylation, methylation, amidation, and the attachment of carbohydrate or lipid moieties, cofactors, and the like. Modified prolyl-tripeptidyl peptidases will hydrolyze SEQ ID NO:25 at the Pro-Yaa peptide bond.

Prolyl peptidases can be obtained by several methods. Isolation of a prolyl-tripeptidyl peptidase present on the surface of a cell producing the peptidase typically requires lysis of the cell followed by purification methods that are well known in the art. Alternatively, cells can be treated with a detergent, for instance Triton X-100, to remove the peptidase from the cell surface. The following are nonlimiting examples of suitable protein purification procedures: fractionation on immunoaffinity, ion-exchange, hydroxyapatite, Phenyl-Sepharose HP, MonoQ HR 5/5, or MonoP columns; ethanol precipitation; reverse phase HPLC; chromatography on silica or on an ion-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75. Preferably, isolation of a prolyl-tripeptidyl peptidase from *P. gingivalis* is accomplished using a combination of hydroxyapatite, Phenyl-Sepharose HP, MonoQ HR 5/5 and MonoP column chromatography steps as described herein.

Prolyl peptidases can also be isolated from organisms other than *P. gingivalis*. Other organisms can express a prolyl-tripeptidyl peptidase that is encoded by a coding region having similarity to the PTP-A coding region. A "coding region" is a linear form of nucleotides that encodes a polypeptide, usually via mRNA, when placed under the control of appropriate regulatory sequences. The boundaries of a coding region are generally determined by a translation start codon at its 5' end and a translation stop codon at its 3' end. "Regulatory region" refers to a nucleic acid fragment that regulates expression of a coding region to which a regulatory region is operably linked. Non limiting examples of regulatory regions include promoters, transcription initiation sites, translation start sites, translation

stop sites, and terminators. "Operably linked" refers to a juxtaposition wherein the components so described are in a relationship permitting them to function in their intended manner. A regulatory element is "operably linked" to a coding region when it is joined in such a way that expression of the coding region is achieved under conditions compatible with the regulatory region. Alternatively, other organisms can express a prolyl-tripeptidyl peptidase from a recombinant coding region encoding the peptidase. The identification of similar coding regions in other organisms can be accomplished as described herein. A prolyl-tripeptidyl peptidase can be isolated using purification methods that are well known in the art.

Alternatively, the peptidase can be chemically synthesized using methods that are well known in the art including, for instance, solid phase synthesis. Examples of, for instance, coding and regulatory regions are described herein.

The expression of a prolyl-tripeptidyl peptidase by an organism other than *P. gingivalis* can be detected using specific substrates of the general formula $\text{NH}_2\text{-Xaa-Xaa-Pro-LG}$ or $\text{NH}_2\text{-Xaa-Xaa-Pro-Yaa}$ (SEQ ID NO:41), where LG is a leaving group. The leaving group can be a chromogenic or fluorogenic group known to the art. The expression of a prolyl-tripeptidyl peptidase by an organism and subsequent cleavage of a specific substrate results in a free amino acid or a free leaving group, each of which can be assayed using techniques known to those of skill in the art. Other methods can be based on immunogenic properties of PTP-A, for instance immunoassays and histochemistry, the detection of mRNA, and PCR related methods, all of which are known to one of skill in the art.

As described in the Examples, the amino acid sequence of the amino-terminal end of a PTP-A fragment was used to identify the nucleotide sequence of the PTP coding region. The nucleotide sequence was present in a publically available database containing the nucleotide sequence of the partially finished *P. gingivalis* W83 genome. However, even though the nucleotides that encode the *P. gingivalis* PTP-A were known, there was no indication that the nucleotides were in fact transcribed and translated. The data obtained from the database only contained the nucleotide sequence of a genomic clone; there was no disclosure that the nucleotides did or did not contain an open reading frame. Moreover, there is little data known to the art regarding regulatory regions required for either the transcription or the translation of a nucleotide sequence in *P. gingivalis*.

Thus, a person of ordinary skill, having the nucleotide sequence of the genomic clone, would not be able to predict that the open reading frame encoding PTP-A was transcribed or translated. Moreover, even if there was a suggestion that the open reading frame was both transcribed and translated, there is no suggestion that the polypeptide encoded by the open reading frame would have the novel activity of PTP-A.

Accordingly, the present invention is directed to a nucleic acid fragment encoding a polypeptide, particularly a prolyl-tripeptidyl peptidase, active analog, active fragment, or active modification thereof. The nucleic acid fragment can have a nucleotide sequence as shown in SEQ ID NO:38. Alternatively, nucleic acid fragments of the invention include those whose complement hybridize to SEQ ID NO:38 under standard hybridization conditions as described herein. During hybridization the entire nucleotide sequence of the complement can hybridize with SEQ ID NO:38. Preferably, at least about 20 nucleotides of the complement hybridize with SEQ ID NO:38, more preferably at least about 50 nucleotides, most preferably at least about 100 nucleotides.

Alternatively, the nucleic acid fragment can have a nucleotide sequence encoding a polypeptide having the amino acid sequence shown in SEQ ID NO:30. An example of the class of nucleotide sequences encoding such a polypeptide is SEQ ID NO:38. This class of nucleotide sequences is large but finite, and the nucleotide sequence of each member of the class can be readily determined by one skilled in the art by reference to the standard genetic code.

The identification of similar coding regions in other organisms can be accomplished by screening individual wild-type microorganisms for the presence of nucleotide sequences that are similar to the coding region of PTP-A, which is shown in SEQ ID NO:38. Screening methods include, for instance, hybridization of a detectably labeled probe with a nucleic acid fragment.

Standard hybridizing conditions are a modification of the conditions used by Church et al. ((1984) *Proc. Natl. Acad. Sci. USA* 81, 1991): 0.5 M phosphate buffer, pH 7.2, 7 % SDS, 10 mM EDTA, at 68°C, and three washes, each for 20 minutes in 2x SSC, 0.1 % SDS, at 65°C. Preferably, a probe will hybridize to the nucleotide sequence set forth in SEQ ID NO:38 under standard hybridizing conditions. Generally the probe does not have to be complementary to all the

nucleotides of the nucleic acid fragment as long as there is hybridization under the above-stated conditions.

“Complement” and “complementary” refer to the ability of two single stranded nucleic acid fragments to base pair with each other, where an adenine on one nucleic acid fragment will base pair to a thymine on a second nucleic acid fragment and a cytosine on one nucleic acid fragment will base pair to a guanine on a second nucleic acid fragment. Two nucleic acid fragments are complementary to each other when a nucleotide sequence in one nucleic acid fragment can base pair with a nucleotide sequence in a second nucleic acid fragment. For instance, 5'-ATGC and 5'-GCAT are complementary. The term complement and complementary also encompasses two nucleic acid fragments where one nucleic acid fragment contains at least one nucleotide that will not base pair to at least one nucleotide present on a second nucleic acid fragment. For instance the third nucleotide of each of the two nucleic acid fragments 5'-ATTGC and 5'-GCTAT will not base pair, but these two nucleic acid fragments are complementary as defined herein. Typically two nucleic acid fragments are complementary if they hybridize under the standard conditions referred to herein.

Preferred probes are nucleic acid fragments complementary to a coding region or another nucleotide sequence that encodes a prolyl-tripeptidyl peptidase. For instance, a probe can comprise a consecutive series of nucleotides complementary to a portion of SEQ ID NO:38. Preferably a probe is at least about 18 bases, more preferably at least about 21 bases, and most preferably at least about 24 bases in length. Particularly preferred probes are

TTCGATCCGGCAAAGAAATATCCTGTTATTGTCTATGTTTACGGAGGAC
CT (SEQ ID NO:36,
GTGGATGCCGATAGAATAGGAGTACATGGCTGGAGCTATGGTGGCTTT
(SEQ ID NO:37, and SEQ ID NO:38. Methods of detectably labeling a probe are well known to the art.

The nucleic acid fragment that is identified by the probe is further analyzed to determine if it encodes a polypeptide with amidolytic activity of the Pro-Yaa

peptide bond on a target polypeptide of the general formula $\text{NH}_2\text{-Xaa-Xaa-Pro-Yaa-(Xaa)}_n$ (SEQ ID NO:25). Another method for screening individual microorganisms for the presence of nucleotide sequences that are similar to the coding regions of the present invention is the polymerase chain reaction (PCR).

5 Individual wild-type microorganisms containing nucleic acid fragments encoding a prolyl-tripeptidyl peptidase can also be identified using antibody. Preferably the antibody is directed to PTP-A. The production of antibodies to a particular polypeptide is known to a person of skill in the art, and is further detailed herein.

10 The use of hybridization of a probe to a coding region present in individual wild-type microorganisms can be used as a method to identify a coding region identical or similar to a coding region present in SEQ ID NO:38. The coding region can then be isolated and ligated into a vector as described below. Two nucleic acid sequences are "similar" if the two nucleic acid sequences can be aligned so that the
15 number of identical amino acids along the lengths of their sequences are optimized. Preferably, two nucleotide acid sequences have, in increasing order of preference, preferably at least about 90 %, at least about 92 %, at least about 94%, at least about 96%, most preferably at least about 98% identity.

As mentioned above, a nucleic acid fragment of the invention can be
20 inserted in a vector. Construction of vectors containing a nucleic acid fragment of the invention employs standard ligation techniques known in the art. See, e.g., Sambrook et al, *Molecular Cloning: A Laboratory Manual.*, Cold Spring Harbor Laboratory Press (1989) or Ausubel, R.M., ed. *Current Protocols in Molecular Biology* (1994). A vector can provide for further cloning (amplification of the
25 nucleic acid fragment), i.e., a cloning vector, or for expression of the polypeptide encoded by the coding region, i.e., an expression vector. The term vector includes, but is not limited to, plasmid vectors, viral vectors, cosmid vectors, or artificial chromosome vectors. Typically, a vector is capable of replication in a bacterial host, for instance *E. coli*. Preferably the vector is a plasmid.

30 Selection of a vector depends upon a variety of desired characteristics in the resulting construct, such as a selection marker, vector replication rate, and the like. Suitable plasmids for expression in *E. coli*, for example, include pUC(X), pKK223-3, pKK233-2, pTrc99A, and pET-(X) wherein (X) denotes a vector family in which

numerous constructs are available. pUC(X) vectors can be obtained from Pharmacia Biotech (Piscataway, NH) or Sigma Chemical Co. (St. Louis, MO). pKK223-3, pKK233-2 and pTrc99A can be obtained from Pharmacia Biotech. pET-(X) vectors can be obtained from Promega (Madison, WI) Stratagene (La Jolla, CA) and Novagen (Madison, WI). To facilitate replication inside a host cell, the vector preferably includes an origin of replication (known as an "ori") or replicon. For example, ColE1 and P15A replicons are commonly used in plasmids that are to be propagated in *E. coli*.

An expression vector optionally includes regulatory regions operably linked to the coding region. The invention is not limited by the use of any particular promoter, and a wide variety are known. Promoters act as regulatory signals that bind RNA polymerase in a cell to initiate transcription of a downstream (3' direction) coding region. The promoter used in the invention can be a constitutive or an inducible promoter. It can be, but need not be, heterologous with respect to the host cell. Preferred promoters for bacterial transformation include *lac*, *lacUV5*, *tac*, *trc*, T7, SP6 and *ara*.

An expression vector can optionally include a Shine Dalgarno site (e.g., a ribosome binding site), and a start site (e.g., the codon ATG) to initiate translation of the transcribed message to produce the enzyme. It can also include a termination sequence to end translation. A termination sequence is typically a codon for which there exists no corresponding aminoacyl-tRNA, thus ending polypeptide synthesis. The nucleic acid fragment used to transform the host cell can optionally further include a transcription termination sequence. The *rrnB* terminators, which is a stretch of DNA that contains two terminators, T1 and T2, is an often used terminator that is incorporated into bacterial expression systems (J. Brosius et al., (1981) *J. Mol. Biol.* 148 107-127).

The nucleic acid fragment used to transform the host cell optionally includes one or more marker sequences, which typically encode a polypeptide that inactivates or otherwise detects or is detected by a compound in the growth medium. For example, the inclusion of a marker sequence can render the transformed cell resistant to an antibiotic, or it can confer compound-specific metabolism on the transformed cell. Examples of a marker sequence are sequences that confer resistance to kanamycin, ampicillin, chloramphenicol, and tetracycline.

Antibodies can be produced to a polypeptide having the sequence of SEQ ID NOs:30, 43, 44 or 45, or a polypeptide having a percentage amino acid identity as described herein. Alternatively, antibodies can be made to an antigenic analog, antigenic fragment, or antigenic modification of a polypeptide having the sequence of SEQ ID NOs:30, 43, 44 or 45. An antigenic analog, antigenic fragment, or antigenic modification of a polypeptide having SEQ ID NOs:30, 43, 44 or 45 is one that generates an immune response in an animal. Antigenic analogs of a polypeptide having SEQ ID NOs:30, 43, 44 or 45 include prolyl peptidases having amino acid substitutions that do not eliminate peptide antigenicity in an animal. Substitutes for an amino acid may be selected from other members of the class to which the amino acid belongs, as described herein. Fragments of a prolyl peptidase of the invention include prolyl peptidases containing deletions or additions of one or more contiguous or noncontiguous amino acids such that the resulting polypeptide will generate an immune response in an animal. An example of a fragments of a prolylpeptidase is a catalytic domain. Modified prolyl peptidases include prolyl peptidases that are chemically and enzymatically derivatized at one or more constituent amino acids, including side chain modifications, backbone modifications, and N- and C- terminal modifications including acetylation, hydroxylation, methylation, amidation, and the attachment of carbohydrate or lipid moieties, cofactors, and the like.

Accordingly, an aspect of the invention is an immunogenic composition comprising an isolated prolyl peptidase, or an antigenic analog, antigenic fragment, or antigenic modification thereof, preferably a prolyl tripeptidyl-peptidase. The prolyl tripeptidyl-peptidase preferably has amidolytic activity for cleavage of the Pro-Yaa peptide bond present in a target polypeptide with the general formula $\text{NH}_2\text{-Xaa-Xaa-Pro-Yaa-(Xaa)}_n$ (SEQ ID NO:25), wherein the amidolytic activity is measured at a prolyl tripeptidyl-peptidase:target polypeptide ratio of at least about 1:100 to no greater than about 1:1,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours.

The immunogenic composition can further include excipients or diluents that are pharmaceutically acceptable as carriers and compatible with the immunogenic composition. The term "pharmaceutically acceptable carrier" refers to a carrier(s) that is "acceptable" in the sense of being compatible with the other

ingredients of a composition and not deleterious to the recipient thereof. Suitable excipients are, for example, water, saline, dextrose, glycerol, ethanol, or the like, and combinations thereof. In addition, if desired, the immunogenic composition may contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents, and/or adjuvants which enhance the effectiveness of the immune-stimulating composition.

The immunogenic composition can be used in a method for protecting an animal from a disease caused by *P. gingivalis*. This method includes administering the immunogenic composition and eliciting antibodies to a prolyl peptidase, antigenic analog, antigenic fragment, or antigenic modification. The diseases that can be treated in this manner include periodontal diseases, which includes gingivitis and periodontitis. Clinical hallmarks of periodontitis include loss of tooth attachment and periodontal pocket formation.

Alternatively and preferably, periodontal diseases can be treated by the use of inhibitors of a prolyl peptidase. An inhibitor of a prolyl peptidase, preferably a prolyl tripeptidyl-peptidase, can be present in a composition that preferably contains a pharmaceutically acceptable carrier. For instance, inhibitors can be applied systemically, subgingivally (e.g., subgingival irrigation) and/or by controlled release delivery directly into the periodontal pocket using methods well known to the art (see, e.g., Kornman, K., (1993) *J. Periodontol.* 64, 782-791). Preferably, an inhibitor is applied subgingivally or by controlled release delivery.

The prolyl peptidases, active analogs, fragments, and modifications thereof can be used in a method of reducing growth of bacteria *in vitro* or *in vivo*. Preferably, the bacteria is a periodontal pathogen, i.e., a bacterial pathogen that causes periodontal disease, more preferably the bacteria is *P. gingivalis*. The inability of asaccharolytic *P. gingivalis* to utilize free amino acids makes the bacterium entirely dependant on an external peptide supply. The action of the polypeptides of the invention may be required for bacterial growth, and inhibition of the polypeptides of the invention may inhibit the *in vivo* growth of organisms, including *P. gingivalis*. The method includes decreasing the amount of dipeptides and/or tripeptides (e.g., the result of cleavage of SEQ ID NO:25 by a prolyl-tripeptidyl peptidase) and the amount of free amino acids that result from further cleavage of the dipeptides and/or tripeptides present by inhibiting a prolyl

peptidase, active analog, active fragment, or active modification thereof, such that the amount of dipeptides and/or tripeptides generated by the polypeptides is decreased. The amount of dipeptides and/or tripeptides is decreased relative to the amount of dipeptides and/or tripeptides present in the absence of the inhibitor.

- 5 Preferably, the amount of dipeptides and/or tripeptides generated is decreased by an inhibitor, a monoclonal antibody that inhibits the prolyl peptidase, or polyclonal antibodies that inhibit the prolyl peptidase, more preferably, the amount of dipeptides and/or tripeptides generated is decreased by an inhibitor. Preferably, an inhibitor acts to inhibit a polypeptide of the invention, preferably a prolyl peptidase,
10 by blocking the active site of the polypeptide. The polypeptide can be present on the surface of the bacteria or secreted into the environment, preferably the polypeptide is present in the surface of the bacteria.

- The present invention is also directed to a method of developing an inhibitor of a prolyl peptidase, active analog, active fragment, or active
15 modification thereof, preferably a prolyl-tripeptidyl peptidase. The method includes identifying a molecule that inhibits the amidolytic activity of the prolyl peptidase. This can be accomplished by, for instance, incubating the prolyl peptidase with a candidate molecule under conditions that promote amidolytic activity of the prolyl peptidase and determining if the amidolytic activity of the
20 prolyl peptidase is decreased relative to the amidolytic activity in the absence of the molecule. The amidolytic activity can be measured by cleavage of the Pro-Yaa peptide bond present in the target polypeptide SEQ ID NO:25 as described herein. One method of developing an inhibitor includes using the target peptide SEQ ID NO:25 and replacing the Xaa residues with modified amino acids. It is expected
25 that some modified amino acids will cause the target peptide to act as an inhibitor.

EXAMPLES

- The present invention is illustrated by the following examples. It is to be understood that the particular examples, materials, amounts, and procedures are to
30 be interpreted broadly in accordance with the scope and spirit of the invention as set forth herein.

Example 1

Materials

Diisopropylfluorophosphate (DFP), leupeptin and 3,4-dichloroisocoumarin, were purchased from Calbiochem (La Jolla, CA). Antipain, iodoacetamide, substance P, bradykinin and bradykinin related peptides, were obtained from Sigma. Other peptides used in this study were synthesized at the Molecular Genetic Instrumental Facility (University of Georgia, Athens, GA) using Fmoc protocol with an advanced ChemTech MPS350 automated synthesizer. H-Ala-Phe-Pro-pNA, H-Gly-Pro-pNA, Z-Gly-Pro-pNA, Z-Ala-Pro-pNA, and H-Pro-pNA (where pNA is p- Nitroanilide; Z is benzyloxycarbonyl; and H is hydrogen and denotes an unblocked amino-terminal group) were obtained from Bachem (King of Prussia, PA). Prolinal was kindly provided by Dr. James Powers (Georgia Institute of Technology, Atlanta) and cystatin C by Dr. Magnus Abrahamson (University of Lund, Sweden).

Methods

Source and Cultivation of Bacteria— *P. gingivalis* HG66 was obtained from Dr. Roland Arnold (University of North Carolina, Chapel Hill), while the strains W50 (ATCC 53978) and ATCC 33277 were obtained from the ATCC. All cells were grown as described previously (Chen, Z., et al., (1992) *J. Biol. Chem.* 267, 18896-18901).

Enzyme Activity Assays— Routinely, the tripeptidyl peptidase amidolytic activity was measured with H-Ala-Phe-Pro-pNA (1mM) in 0.2 M HEPES (N-2-hydroxyethylpeperazine,N'-2-ethansulfonic acid), pH 7.5 at 37°C. The concentration of enzyme was 0.1 nM to 1 nM. The assay was performed in a total volume of 0.2 ml on microplates, and the initial turnover rate was recorded at 405 nm using a microplate reader (Spectramax Molecular Devices, Sunnyvale, CA). In inhibition studies, the enzyme was first preincubated with inhibitor for 15 min at 37°C, substrate added, and residual activity recorded after 5 minutes to 30 minutes. H-Gly-Pro-pNA, Z-Ala-Pro-pNA, Z-Gly-Pro-pNA and H-Pro-pNA (1 mM final concentration) were assayed in the same manner.

Protein Determination—Protein concentration was determined using the BCA reagent kit (Sigma, St. Louis, MO), using bovine serum albumin as a standard.

Localization of Tripeptidyl-Peptidase Activity—Cultures of *P. gingivalis* HG66, W50 and ATCC 33277, at different phases of growth, were subjected to the following fractionation procedure. The cells were removed by centrifugation (10,000 x g, 30 minutes), washed twice with 10 mM Tris, 150 mM NaCl, pH 7.4, resuspended in 50 mM Tris, pH 7.6, and disintegrated by ultrasonication in an ice bath at 1500 Hz for 5 cycles (5 minutes sonication/5 minutes brake). Unbroken cells and large debris were removed by centrifugation (10,000 x g, 30 minutes) and the opalescent supernatant subjected to ultracentrifugation (150,000 x g, 120 minutes), yielding a pellet containing bacterial membranes and a supernatant which was considered as membrane-free cell extract. All fractions, as well as the full culture, culture medium, and full culture after sonication, were assayed for amidolytic activity against H-Ala-Phe-Pro-pNA.

Enzyme Purification—All purification steps were performed at 4°C except for FPLC separations, which were carried out at room temperature. Cells were harvested by centrifugation (6,000 x g, 30 minutes), washed with 50 mM potassium phosphate buffer, pH 7.4, and resuspended in the same buffer (150 ml per 50 gram of cells wet weight). Triton X-100 (10% volume/volume in H₂O) was added slowly to the bacterial cell suspension to a final concentration of 0.05%. After 120 minutes of gentle stirring, unbroken cells were removed by centrifugation (28,000 x g, 60 minutes). Proteins in the supernatant were precipitated with cold acetone (-20°C) added to a final concentration of 60% and collected by centrifugation. The pellet was redissolved in 50 mM potassium phosphate buffer, pH 7.0, and extensively dialyzed against 20 mM potassium phosphate, pH 7.0, containing 0.02% sodium azide. The dialyzed fraction was clarified by centrifugation (28,000 x g, 30 min) and applied to a hydroxyapatite column (BioRad, Melville, NY) equilibrated with 20 mM potassium phosphate, pH 7.0, at a flow rate of 20 ml/hour. After equilibration, the column was washed until the A₂₈₀ fell to zero. Bound proteins were eluted with a gradient from 20-300 mM potassium phosphate and fractions (7 ml) analyzed for dipeptidyl- and tripeptidyl-peptidase activity using H-Gly-Pro-pNA and H-Ala-Phe-Pro-pNA, respectively. The activity against the latter

substrate was pooled, saturated with 1 M ammonium sulfate, clarified by centrifugation, and directly loaded onto a Phenyl-Sepharose HP (Pharmacia, Piscataway, NJ) column equilibrated with 50 mM potassium phosphate, pH 7.0, containing 1 M ammonium sulfate. The column was washed with two volumes of equilibration buffer, followed by buffer containing 0.5 M ammonium sulfate, and developed with a descending gradient of ammonium sulfate from 0.5 to 0 M. Active fractions were pooled, extensively dialyzed against 20 mM Tris, pH 7.5, and applied to a MonoQ HR 5/5 FPLC column equilibrated with the same buffer. The column was washed with 5 volumes of equilibration buffer at 1.0 ml/minute, following which bound proteins were eluted with a gradient of 0- 300 mM NaCl. The active fractions were pooled, dialyzed against 25 mM Bis-Tris, pH 6.3, and subjected to chromatofocusing on a MonoP FPLC column equilibrated with Bis-Tris buffer, using a pH gradient developed with 50 ml of 10x diluted Polybuffer 74 (Pharmacia), adjusted to a pH of 4.0.

Electrophoretic Techniques—The SDS-PAGE system of Schagger and von Jagow (Schagger, H., and von Jagow, G. (1987) *Anal. Biochem.* 166, 368-379), was used to monitor enzyme purification and estimate the enzyme molecular mass. For amino-terminal sequence analysis, proteins resolved in SDS-PAGE were electroblotted to polyvinylidene difluoride membranes using 10 mM CAPS, pH 11, 10% methanol (Matsudaira, P. (1987) *J. Biol. Chem.* 262, 10035-10038). The membrane was washed thoroughly with water and stained with Coomassie Blue G250. The blot was air dried, and protein bands cut out and subjected to NH₂-terminal sequence analysis with an Applied Biosystems 491 Protein Sequencer using the program designed by the manufacturers.

Enzyme Fragmentation—The purified prolyl tripeptidyl peptidase (PTP-A) was partially denatured by incubation in 6 M urea in 0.02 M Tris, pH 7.6, for 60 minutes. Low molecular mass gingipain R (RgpB) (Potempa, J., et al. (1995) *Prospect. Drug Discovery and Design* 2, 445-458) from *P. gingivalis* was then added to make an enzyme:substrate molar ratio of 1:100. The reaction mixture was made in 1 mM cysteine and the sample incubated overnight at 37°C. Generated peptides were separated by reverse-phase HPLC using a μ Bondapak C-18 column (3.9 x 300 mm) (Waters, Millford, MA). Peptides were eluted with 0.1% trifluoroacetic acid and acetonitrile containing 0.08% trifluoroacetic acid, using a

gradient from 0 to 80% acetonitrile over 60 minutes. Peptides were monitored at 220 nm and collected manually.

For determination of the active site serine residue and to confirm that the purified enzyme was a serine peptidase, 100 µg of purified PTP-A was first
5 incubated with 170 µCi of [1,3-³H]DFP (Amersham, Arlington Heights, IL) for 30 minutes at 25°C in 20 mM HEPES, pH 7.5. The reaction was quenched by addition of cold DFP to a final concentration of 10 mM and the radiolabelled material analyzed by SDS-PAGE, followed by autoradiographic analysis. The gel was dehydrated, soaked in PPO solution for 2 hours, dried, and the DFP-binding
10 proteins detected by fluorography after an exposure time of 96 hours on X-ray film (XAR; Kodak, Rochester, NY). The bulk of radiolabelled protein was subjected to proteolytic fragmentation with RgpB and peptides obtained separated by reverse-phase HPLC as described above. Radioactivity in each peptide fraction was measured using a β liquid scintillation counter, and the labeled peptide, as well as
15 other selected peptides were subjected to sequence analysis.

Identification of the PTP-A Gene— The database containing the unfinished *P. gingivalis* W83 genome, available from The Institute for Genomic Research, was searched for the presence of nucleotide sequences corresponding to the NH₂-terminal and the internal PTP-A amino acid sequences using the TBLASTN
20 algorithm, BLAST version 2.0.8, and the default values for all parameters (Altschul, S.F., et al., (1997) *Nucleic Acid Res.* 25, 3389-3402). An identified clone gnl | TIGR | *P. gingivalis*_126 was retrieved from The Institute for Genomic Research data base (<http://www.tigr.org>). The position of the PTP-A gene was localized using the NCBI open reading frame (ORF) finder (available from the
25 National Center for Biotechnology Information, at <http://www.ncbi.nlm.nih.gov/gorf/gorf.html>). The amino acid sequence, obtained by conceptual translation of the entire ORF, was further used for homology screening by use of the NCBI BLAST search tool.

Enzyme Specificity— Peptides were incubated with 1 µg PTP-A at an
30 enzyme:substrate molar ratio of 1:100 for 3 hours or 24 hours in 50 µl of 200 mM HEPES, pH 7.5, at 37°C, and the reaction stopped by acidification with trifluoroacetic acid. The samples were then subjected to reverse-phase high

pressure liquid chromatography using a μ Bondapak C-18 column (3.9 x 300 mm) (Waters, Millford, MA) and an acetonitrile gradient (0-80 % in 0.075% trifluoroacetic acid in 50 min). Each peak, detected at 220 nm, was collected, lyophilized, re-dissolved in 50% (volume/volume) methanol, 0.1% acetic acid and subjected to analysis by mass spectrometry.

Mass Spectrometry—A Finnigan MAT 95S, sector mass spectrometer (Finnigan MAT, Bremen, Germany) equipped with an electrospray source (ESI) was used operated essentially as described previously (Stenfors, C., et al., (1997) *J. Biol. Chem.* 272, 5747-5751). Peptides were identified by fitting of the obtained spectra to specific sequences using an Internet application program MsFit available at <http://falcon.ludwig.ucl.ac.uk/msfit.html>.

Example 2

Enzyme Localization, Purification and Initial Characterization

Analysis of amidolytic activity against H-Ala-Phe-Pro-pNA in several fractions of *P. gingivalis* HG66, W50 and ATCC 33277 clearly indicated that an enzyme(s) with prolyl tripeptidyl-peptidase activity is localized on the cell surface in all strains tested with less than 5% of the total activity being found in the medium regardless of the growth phase of the bacterial culture. Cell associated enzyme was easily detached from the bacterial surface by treatment with a low concentration (0.05%) of Triton X-100. This procedure released more than 85-90% of activity in a soluble form. Subsequent acetone precipitation of proteins in the Triton X-100 fraction successfully separated the activity from pigment which remained in solution. The redissolved protein fraction, after dialysis, was applied to hydroxyapatite (100 ml) equilibrated with 20 mM potassium phosphate buffer pH 7.0. The elution was carried out with 20 mM potassium phosphate buffer pH 7.0, using a phosphate gradient from 20 mM to 300 mM at flow rate 20 ml/h. At this step substantial separation of the PTP-A activity from both the DPP IV and bulk protein was achieved (Fig. 1a). Further purification performed by subsequent chromatography steps including Phenyl-Sepharose (Fig. 1b), MonoQ (Fig. 1c) and MonoP columns (Fig. 1d), resulted in the isolation of purified enzyme.

Phenyl-Sepharose HP (25 ml) was equilibrated with 50 mM potassium phosphate, 1M ammonium sulfate, pH 7.0, at flow rate 30 ml/h. The column was

washed with two volumes of equilibration buffer and a step gradient of 0.5 M ammonium sulfate was applied, following which a descending gradient of 0.5 to 0 M ammonium sulfate was applied. The PTP-A containing fractions were extensively dialyzed against 20 mM Tris-HCl, pH 7.0, and concentrated by ultrafiltration. The concentrated PTP-A containing fractions were applied to a MonoQ column equilibrated with the same buffer. The column was washed with 5 volumes of equilibration buffer, following which bound protein was eluted with a gradient of 0-300 mM NaCl. The concentrated fraction of PTP-A from the MonoQ column was equilibrated with 25 mM Bis-Tris, pH 6.3, and loaded on a MonoP column equilibrated with the same buffer. A pH gradient was developed using 50 ml of Polybuffer 74, with the pH adjusted to 4.0.

Significantly, the chromatography step on the MonoP column yielded the A_{280} profile much sharper than the activity peak. Although this imperfect overlap of protein and activity may suggest that the protein component does not represent the active enzyme, the rest of data argues with such a contention. This apparent contradiction may be likely explained by the enzyme inhibition by the reaction product of H-Ala-Phe-Pro-pNA hydrolysis but this possibility has not been explored. The yield of protein and activity recovery in a typical purification procedure is summarized in Table 1.

Table 1. Purification of the PTP- A from *P. gingivalis*

Step	Volume (ml)	Protein (mg)	Total activity*	Specific activity (units/mg)	Purification fold	Yield (%)
5	Triton X-100 extract after centrifugation					
	200	1200	757 673	642	1	100
	Acetone precipitate					
10	50	600	537 622	896	1.4	71
	Hydroxyapatite chromatography					
	50	22	400 039	18 183	28	53
15	Phenyl-Sepharose					
	48	10	312 505	31 250	48	41
	3	1.5	244 828	163 218	254	32
MonoQ						
MonoP						
	4	0.7	188 400	269 142	420	25

* Based on the enzymatic activity using H-Ala-Phe-Pro-pNA where one unit = mOD/min/1ml

SDS-PAGE analysis of the purified enzyme revealed the presence of two protein bands with apparent molecular masses of 81.8 and 75.8 kDa, respectively (Fig. 2, lane f). Autoradiography of the enzyme sample radiolabeled with [1,3-³H]DFP (Fig. 2, lane g) clearly indicated that the bands represented either two distinct serine peptidases or different molecular mass forms of the same enzyme. In an attempt to distinguish between these two options, the electrophoretically resolved proteins were subjected to amino terminal sequence analysis. Unfortunately, it was found that the 81.8 kDa form of PTP-A had a blocked N-terminus. In contrast, the sequence NH₂-SAQTTRFSAADLNALMP (SEQ ID NO:23) was found at the N-terminus of the lower molecular mass form of the enzyme. This result led us to the possibility that the 75.8 kDa form of PTP-A was derived from the 81.8 kDa form through proteolytic cleavage of a 6 kDa amino-terminal peptide. To confirm this hypothesis and, in addition, to localize the active site residue within *P. gingivalis* PTP-A, the mixture containing both radiolabeled enzymes was proteolytically fragmented and peptides resolved by reverse-phase HPLC. This procedure yielded only one major radioactive peptide peak, and the purified peptide was found to have a single amino acid sequence: IGVHGWXYGGFMTTNL (SEQ ID NO:24), where X apparently represents the active-site serine residue covalently and irreversibly modified by DFP. These data convincingly indicate that the two protein bands of purified PTP-A represents different forms of the same enzyme. The portion of the purified PTP-A having a truncated N-terminus may be due to cleavage by Lys-specific peptidase and is likely to be an artifact which occurred during the purification procedure. Nevertheless, the proteolytic shedding of membrane bound PTP-A also occurs during cultivation of the bacteria, as indicated by variable amount of soluble activities found in cell free culture media.

Example 3

pH Optimum, Stability and Inhibition Profile

Using the amidolytic activity assay with H-Ala-Phe-Pro-pNA it was found that the enzyme has a broad pH optimum from pH 6.0 to 8.0 and in 0.2 M HEPES, pH 7.6 was stable for at least 12 hours at 25°C or 37°C. PTP-A activity was not affected by class specific synthetic inhibitors of cysteine or metalloproteinases

(Table 2). In contrast, preincubation of the enzyme with DFP or PEFABLOCK resulted in total loss of activity, supporting its classification as a serine peptidase. Surprisingly, however, 3,4-dichloroisocoumarin was only a poor inhibitor, and PMSF, leupeptin, antipain and prolinal had no effect at all. Interestingly, preincubation of PTP-A with iodoacetamide, but not with N-ethylmaleimide, stimulated enzyme amidolytic activity about two-fold. Human plasma inhibitors, such as α_1 -proteinase inhibitor, α_1 -antichymotrypsin and α_2 -macroglobulin did not affect the enzyme activity, nor were they cleaved by PTP-A.

The effect of inhibitors on amidolytic activity of DPP IV was also determined using the same conditions as those used for PTP-A, but using H-Gly-Pro-pNA as a substrate.

Table 2. Effect of inhibitors on the amidolytic activity of PTP-A and DPP IV. Results are for a 15-min incubation at 37 C in 0.2 HEPES pH 7.6, with 1 mM H-Ala-Phe-Pro-pNA as substrate.

	Inhibitor	Concentration	Residual activity of PTP-A, %	Residual activity of DPP IV, %
5	Diisopropyl fluorophosphate	10 mM	0	0
		10 mM	96	20
10	Phenylmethanesulfonyl fluoride	1mg/ml	20	15
		10mg/ml	0	0
	PEFABLOC SC	1 mM	56	100
15	3,4-dichloroisocoumarin	5mM	200	100
	Iodoacetamide	5 mM	100	100
	N-Ethylmaleimide	1 mM	98	100
20	1,10- orthophenanthroline	5 mM	93	100
		0.1 mM	100	100
	EDTA	0.1 mM	100	100
25	Leupeptin	0.1 mM	100	20
	Antipain	10 mM	100	0
30	Prolinal	10 mM	100	30
	Val-Pro	10 mM	100	1
	Ala-Pro			
35	Ala-Gly-Pro			

Example 4

Substrate Specificity

Among several chromogenic substrates tested, including H-Ala-Phe-Pro-pNA, H-Gly-Pro-pNA, Z-Gly-Pro-pNA, Z-Ala-Pro-pNA, H-Pro-pNA, only H-Ala-Phe-Pro-pNA was hydrolyzed by PTP-A indicating a prolyl specific tripeptidyl-peptidase activity. To further confirm this specificity several synthetic peptides composed of 5 to 34 amino acid residues and containing at least one proline residue were tested as substrates for PTP-A. Out of 22 peptides tested only those with a proline residue in the third position from the amino terminal end were cleaved (Table 3), with the significant exception of peptides with adjacent proline residues (peptides 3, 4 and 16). In addition, a free α -amino group was absolutely required for cleavage after the third proline residue as exemplified by resistance to enzymatic hydrolysis of peptide 9, which differs from the peptide 8 only in acylation of the α -amino group of the N-terminal valine residue. Except for these two limitations, the peptide bond -Pro-↓-Yaa- was cleaved at the same rate in all peptides with the general formula $\text{NH}_2\text{-Xaa-Xaa-Pro-Yaa-(Xaa)}_n$ (SEQ ID NO:25), where Xaa represents any amino acid residue while Yaa could be any residue except proline, regardless of the chemical nature of the amino acids and the length of the peptide. In all cases the reaction was completed within 3 hours and prolonged incubation for 24 hours did not affect the pattern of cleavage, confirming the absolute requirement for a proline residue at the third position from the unblocked N-terminus. In addition, these data indicate that the preparation of PTP-A was free of any contamination with either aminopeptidase, dipeptidyl peptidase, or endopeptidase activities.

The cleavage specificity of DPP IV was also determined using the same conditions as those used for PTP-A. The results (Table 3) demonstrate that DPP IV does not cleave between two proline residues.

Table 3. Cleavage specificity of PTP-A and DPP IV on synthetic peptides.

Substrate	Cleavage site	SEQ ID NO:
Peptide 1	H-Arg-Pro-Pro- -Gly-Phe-Ser-Pro-Phe-Arg	1
Peptide 2	H-Arg-Pro-Pro- -Gly-Phe	2
Peptide 3	H-Lys-Arg-Pro-Pro-Gly-Phe-Ser-Pro-Phe-Arg	3
Peptide 4	H-Tyr-Arg-Pro-Pro-Gly-Phe-Ser-Pro-Phe-Arg	4
Peptide 5	H-Arg-Pro-Hyp-Gly-Phe-Ser-Pro-Phe-Arg	5
Peptide 6	H-Arg-Pro- -Lys-Pro- -Gln-Gln-Phe-Phe-Gly-Leu-Met-NH ₂	6
Peptide 7	H-Val-Pro-Pro- -Gly-Glu-Asp-Ser-Lys-Glu-Val-Ala-Ala-Pro-His-Arg-Gln	7
Peptide 8	H-Val-Pro-Pro- -Gly-Glu-Asp-Ser-Lys	8
Peptide 9	Ac-Val-Pro-Pro-Gly-Glu-Asp-Ser-Lys	9
Peptide 10	H-Val-Glu-Pro- -Ile-Pro-Tyr	10
Peptide 11	H-Arg-Gly-Pro- -Phe-Pro-Ile	11
Peptide 12	H-Ala-Arg-Pro- -Ala-D-Lys-amide	12
Peptide 13	H-Pro-Asn-Pro- -Asn-Gln-Gly-Asn-Phe-Ile	13
Peptide 14	H-Arg-His-Pro- -Lys-Tyr-Lys-Thr-Glu-Leu	14
Peptide 15	H-Gly-Val-Pro- -Lys-Thr-His-Leu-Glu-Leu	15
Peptide 16	H-Lys-Gly-Pro-Pro-Ala-Ala-Leu-Thr-Leu	16
Peptide 17	H-Gln-Lys-Gln-Met-Ser-Asp-Arg-Glu-Asn-Asp-Met-Ser-Pro-Ser-Asn-Asn-Val-Val-Pro-Ile-His-Val-Pro-Pro-Thr-Thr-Glu-Asn-Lys-Pro-Lys-Val-Gln	17
Peptide 18	H-Phe-Leu-Arg-Glu-Pro-Val-Ile-Phe-Leu	18
Peptide 19	H-Gly-Ile-Arg-Pro-Tyr-Glu-Ile-Leu-Ala	19
Peptide 20	H-Leu-Pro- -Asp-Leu-Asp-Ser-Ser-Leu-Ala-Ser-Ile-Gln-Glu-Leu-Ser-Pro-Gln-Glu-Pro-Arg-Pro-Pro-Glu-Ala	20
Peptide 21	H-Cys-Leu-Ser-Ser-Gly-Thr-Leu-Pro-Gly-Pro-Gly-Asn-Asp-Ala-Ser-Arg-Glu-Leu-Glu-Ser	21
Peptide 22	H-Lys-Ile-Ala-Gly-Tyr-His-Leu-Glu-Leu	22
Peptide 23	H-Ser-Pro- -Tyr-Ser-Ser-Asp-Thr-Thr	46
Peptide 24	H-Ala-Pro- -Val-Arg-Ser-Leu-Asn-Cys-Thr-Leu-Arg-Asp-Ser-Gln-Gln-Lys	47

| indicates cleavage site mediated by PTP-A

| indicates cleavage site mediated by DPP IV

The lack of cleavage after internal proline residues in the synthetic peptides corresponds well with the absence of any proteolytic activity on several protein substrates including IgA, IgG, albumin, azocasein, carboxymethylated rybonuclease and gelatin. However, the size of substrate, which is a limiting factor in the activity of oligopeptidases (Walter, R., et al., (1980) *Mol. Cell. Biochem.* 30, 111-126), is not restricting in the case of PTP-A, because the enzyme is able to cleave a tripeptide (NH₂-Xaa-Xaa-Pro) from the N-terminus of both human cystatin C and interleukin 6.

Example 5

PTP-A Sequence Analysis

Partial PTP-A amino acid sequence data allowed us to identify the *P. gingivalis* genomic clone gnl | TIGR | *P. gingivalis*_126 in the Unfinished Microbial Genomes data base, TIGR. An ORF corresponding to the PTP-A amino acid sequence was found as indicated by the fact that all sequences of the PTP-A derived peptides obtained by the enzyme polypeptide fragmentation with RgpB were present in the protein primary structure inferred from the nucleotide sequence of the ORF. The 732 amino acid polypeptide with a calculated mass of 82, 266 Da was encoded in this ORF. The homology search performed using the NCBI TBLASTN tool against GenBank+EMBL+DDBJ+PDB databases and subsequent multiple sequence alignments using the ClustalW Multiple Sequence Alignment tool (Fig. 3) indicated that PTP-A is a new member of the prolyl oligopeptidase (S9) family of serine peptidases (Rawlings, N.D., et al., (1991) *Biochem. J.* 279, 907-908).

The sequence GX SXGG (SEQ ID NO:40) is a signature feature for the S9 family of serine peptidases. Within this large and diverse S9 family of evolutionary and functionally related enzymes both from prokaryotes and eukaryotes, PTP-A was most closely related to bacterial dipeptidyl peptidase IV (DPP IV) from *Flavobacterium meningosepticum*, *Xantomonas maltophilus*, and *P. gingivalis*, sharing 31.6%, 30.4%, and 28.5% amino acid sequence identity, respectively. Remarkably, the COOH-terminal region of the PTP-A molecule (residues 502 - 732) shows a significant similarity to the eukaryotic prolyl oligopeptidases with 34% and 33% identity to human DPP IV and mouse fibroblast activation protein (FAP), respectively (Fig. 3). This part of the molecule contains the amino acid

residues which encompass the catalytic triad in all characterized prolyl oligopeptidases, and from the multiple alignments with DPP IV of confirmed active site residues (Kabashima, T., et al., (1995) *Arch. Biochem. Biophys.* 320, 123-128) it is apparent that Ser-603, Asp-678 and His-710 represent the catalytic triad of PTP-A (Fig. 3). Such an inference is further supported by the direct labeling of Ser-603 by DFP. In addition, the computer assisted search for sequential motifs characteristic for transmembrane domains revealed the presence of such a putative region within the N-terminal sequences of PTP-A, with residues 5 to 25 most likely folded into a hydrophobic α -helix responsible for membrane anchoring of this enzyme.

In *P. gingivalis* PTP-A, as well as in DPP IV, all activities are cell surface associated, and it is conceivable that the enzymes are membrane anchored through putative signal sequences which are not cleaved but remain as a membrane spanning domain similar to other members of the prolyl oligopeptidase family. The cell surface localization of di- and tripeptidyl-peptidases suggests a putative physiological function in providing nutrients for growing bacterial cells. Here, the inability of asaccharolytic *P. gingivalis* to utilize free amino acids (Dashper, S.G., et al., *J. Dent Res.* 77, 1133 (Abstract) (1988)) makes the bacterium entirely dependant on an external peptide supply. In this regard, DPP-IV and PTP-A activities are probably very important, if not indispensable, for bacterial growth.

This suggestion is strongly corroborated by the fact that the *P. gingivalis* genome contains three additional genes encoding peptidases homologous with DPP-IV and PTP-A and one related to aminopeptidase B. The peptidases homologous with DPP-IV and PTP-A are referred to as homologs H1 (SEQ ID NO:43), H2 (SEQ ID NO:44), and H3 (SEQ ID NO:45) (Fig. 6). If expressed, each gene product would probably have enzymatic activity because each has a well preserved catalytic triad (Fig. 4). In addition, all of these genes encode a putative signal peptide which may act in providing membrane-anchorage motifs.

Example 6**Influence of Proteinase Inhibitor on *P. gingivalis* Growth**

To evaluate whether *P. gingivalis* growth was influenced by the presence of a peptidase inhibitor, *P. gingivalis* in logphase growth was diluted 1:5 into liquid media and incubated at 37°C. The cell density was monitored by measuring the optical density at 600 nm (OD₆₀₀). When the optical density began to increase, Pefabloc was added at 0.5 mg/ml or at 2.0 mg/ml. The control culture received no Pefabloc. The cultures receiving Pefabloc exhibited decreased growth (Figure 5). The peptidase inhibitor had to be added before the culture reached an OD₆₀₀ of about 0.3 for the peptidase inhibitor to have an effect on growth.

The complete disclosures of all patents, patent applications, publications, and nucleic acid and protein database entries, including for example GenBank accession numbers and EMBL accession numbers, that are cited herein are hereby incorporated by reference as if individually incorporated. Various modifications and alterations of this invention will become apparent to those skilled in the art without departing from the scope and spirit of this invention, and it should be understood that this invention is not to be unduly limited to the illustrative embodiments set forth herein.

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Sequence Listing Free Text

- SEQ ID NOs:1-11: Synthetic peptides
- SEQ ID NO:12: Target peptide
- SEQ ID NOs:13-22: Synthetic peptides
- 25 SEQ ID NO:23: Amino-terminus of the lower molecular mass form of PTP-A.
- SEQ ID NO:24: Amino acid sequence present in PTP-A, where X apparently represents the active-site serine residue covalently and irreversibly modified by DFP.
- 30 SEQ ID NO:25: Target peptide, where Xaa represents a natural or modified amino acid residue, Yaa represents a natural or modified amino acid residue except proline, and N is equal to or greater than 1.
- SEQ ID NO:26: Mouse fibroblast activation protein

- SEQ ID NO:27: Human DPP IV
- SEQ ID NO:28: DPP from *Flavobacterium meningosepticum*
- SEQ ID NO:29: DPP from *P. gingivalis*
- SEQ ID NO:30: *P. gingivalis* PTP-A
- 5 SEQ ID NO:31: Portion of PTP-A
- SEQ ID NO:32: Portion of DPP from *P. gingivalis*
- SEQ ID NO:33: Portion of H1 homolog of *P. gingivalis* DPP
- SEQ ID NO:34: Portion of H2 homolog of *P. gingivalis* DPP
- SEQ ID NO:35: Portion of H3 homolog of *P. gingivalis* DPP
- 10 SEQ ID NOs:36-37: Probes
- SEQ ID NO:38: Nucleotide sequence of coding region encoding PTP-A.
- SEQ ID NO:39: Consensus sequence for clan SC where X is any amino acid and S is the active site serine GXSTXG.
- SEQ ID NO:40: Consensus sequence for family S9 where X is any amino acid and S is the active site serine GXSTGG.
- 15 SEQ ID NO:41: A specific substrate for a prolyl-tripeptidyl peptidase, where Xaa represents a natural or modified amino acid residue, and Yaa represents a natural or modified amino acid residue except proline.
- 20 SEQ ID NO:42: DPP from *P. gingivalis*
- SEQ ID NO:43: H1 homolog of *P. gingivalis* DPP
- SEQ ID NO:44: H2 homolog of *P. gingivalis* DPP
- SEQ ID NO:45: H3 homolog of *P. gingivalis* DPP
- SEQ ID NO:46: Synthetic peptides
- 25 SEQ ID NO:47: Synthetic peptides
- SEQ ID NO:48: Amino terminal sequence of DPP IV

What is claimed is:

1. An isolated prolyl tripeptidyl-peptidase, active analog, active fragment, or active modification thereof having amidolytic activity for cleavage of a peptide bond present in a target polypeptide having at least 4 amino acids, wherein the prolyl tripeptidyl-peptidase:target polypeptide ratio is at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours.
2. An isolated prolyl tripeptidyl-peptidase, active analog, active fragment, or active modification thereof having amidolytic activity at a prolyl tripeptidyl-peptidase:target polypeptide ratio of at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours, and wherein the prolyl tripeptidyl-peptidase is isolated from *P. gingivalis*.
3. The isolated prolyl tripeptidyl-peptidase of claim 2 wherein the peptide cleaved by the isolated prolyl tripeptidyl-peptidase comprises the sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:11, H-Ala-Arg-Pro-Ala-D-Lys-amide, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:25, and SEQ ID NO:37.
4. The isolated prolyl tripeptidyl-peptidase of claim 2 wherein the amino acid sequence of the isolated prolyl tripeptidyl-peptidase comprises the amino acid sequence GXSEXG (SEQ ID NO:39).
5. The isolated prolyl tripeptidyl-peptidase of claim 4 wherein the amino acid sequence of the isolated prolyl tripeptidyl-peptidase comprises the amino acid sequence GXSEXG (SEQ ID NO:40).
6. The isolated prolyl tripeptidyl-peptidase of claim 4 wherein the amino acid sequence of the isolated prolyl tripeptidyl-peptidase comprises SEQ ID NO:30.

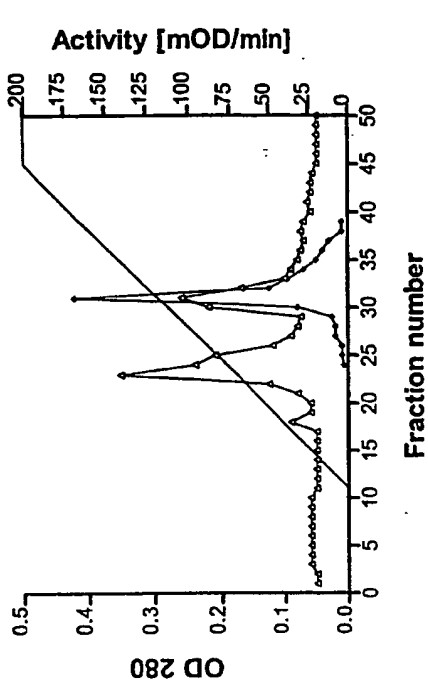
7. An isolated polypeptide, active analog, active fragment, or active modification thereof having amidolytic activity for cleavage of a peptide bond present in a target polypeptide having at least 4 amino acids, wherein the polypeptide:target polypeptide ratio of at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours.
8. An isolated polypeptide comprising an amino acid sequence having a percentage amino acid identity of greater than 35 % with SEQ ID NO:30.
9. An isolated nucleic acid fragment encoding a prolyl-tripeptidyl peptidase, active analog, active fragment, or active modification thereof, having amidolytic activity for cleavage of a peptide bond present in a target polypeptide having at least 4 amino acids, wherein the prolyl tripeptidyl-peptidase:target polypeptide ratio of at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours.
10. The nucleic acid fragment of claim 9 wherein the nucleic acid fragment has a nucleotide sequence comprising SEQ ID NO:38.
11. The nucleic acid fragment of claim 9 wherein a complement of the nucleic acid fragment hybridizes to SEQ ID NO:38 under hybridization conditions of 0.5 M phosphate buffer, pH 7.2, 7 % SDS, 10 mM EDTA, at 68°C, followed by three for 20 minutes washes in 2x SSC, and 0.1 % SDS, at 65°C, wherein at least about 20 nucleotides of the complement hybridize.
12. An isolated nucleic acid fragment encoding a polypeptide wherein the polypeptide comprises an amino acid sequence having a percentage amino acid identity of greater than 35 % with SEQ ID NO:30.
13. A method of identifying an inhibitor of a prolyl-tripeptidyl peptidase, active analog, active fragment, or active modification thereof, comprising identifying a molecule that inhibits the amidolytic activity of the prolyl-

tripeptidyl peptidase by incubating the prolyl-tripeptidyl peptidase with the molecule under conditions that promote amidolytic activity of the prolyl-tripeptidyl peptidase and determining if the amidolytic activity of the prolyl-tripeptidyl peptidase is inhibited relative to the amidolytic activity in the absence of molecule.

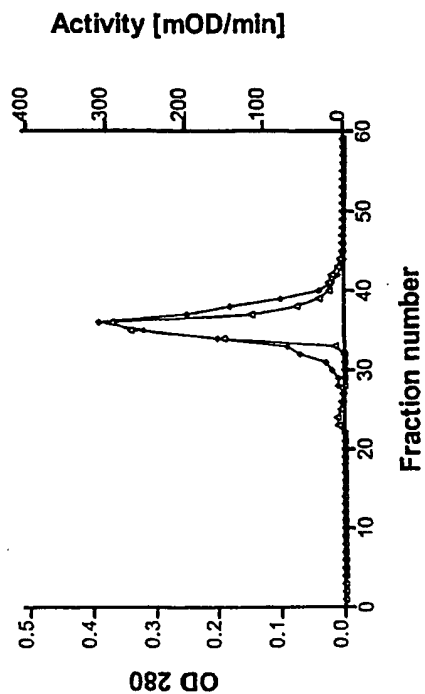
14. A method of reducing growth of a bacterium comprising inhibiting a prolyl tripeptidyl-peptidase, active analog, active fragment, or active modification thereof, by contacting the prolyl tripeptidyl-peptidase with an inhibitor of the prolyl tripeptidyl-peptidase.
15. A method for protecting an animal from a periodontal disease caused by *P. gingivalis* comprising administering to the animal the inhibitor of claim 14 wherein the disease is selected from the group consisting of gingivitis and periodontitis.
16. The method of claim 15 wherein the inhibitor is administered by a method selected from the group consisting of subgingival application and controlled release delivery.
17. A method of reducing growth of a bacterium comprising inhibiting a prolyl dipeptidyl-peptidase, active analog, active fragment, or active modification thereof, by contacting the prolyl dipeptidyl-peptidase with an inhibitor of the prolyl dipeptidyl-peptidase.
18. An immunogenic composition comprising an isolated prolyl tripeptidyl-peptidase, or an antigenic analog, antigenic fragment, or antigenic modification thereof, the prolyl tripeptidyl-peptidase having amidolytic activity for cleavage of a peptide bond present in a target peptide having at least 4 amino acids, wherein the prolyl tripeptidyl-peptidase:target polypeptide ratio is at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours.
19. The immunogenic composition of claim 18 further comprising an adjuvant.

20. A composition comprising an inhibitor of an isolated prolyl tripeptidyl-peptidase and a pharmaceutically acceptable carrier.
21. A dipeptidyl peptidase having an amino acid sequence comprising SEQ ID NO:43.
22. A dipeptidyl peptidase having an amino acid sequence comprising SEQ ID NO:44.
23. A dipeptidyl peptidase having an amino acid sequence comprising SEQ ID NO:45.

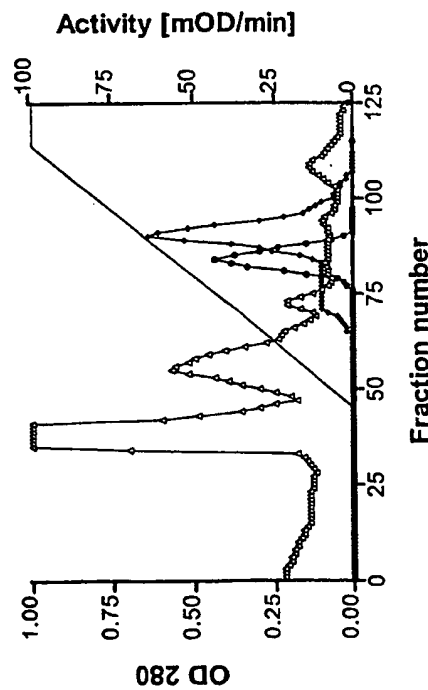
Fig 1



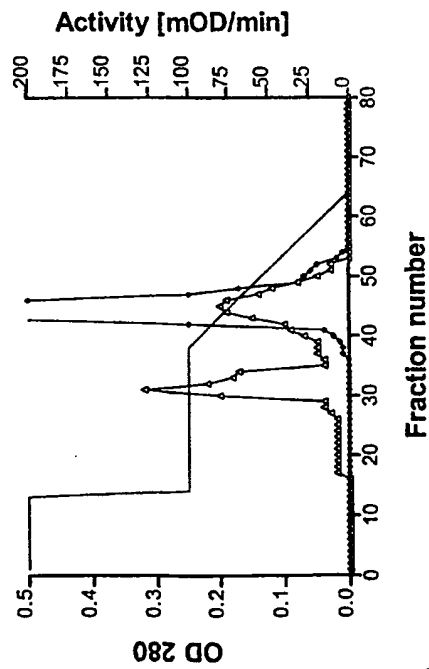
c)



d)



a)



b)

Fig. 2

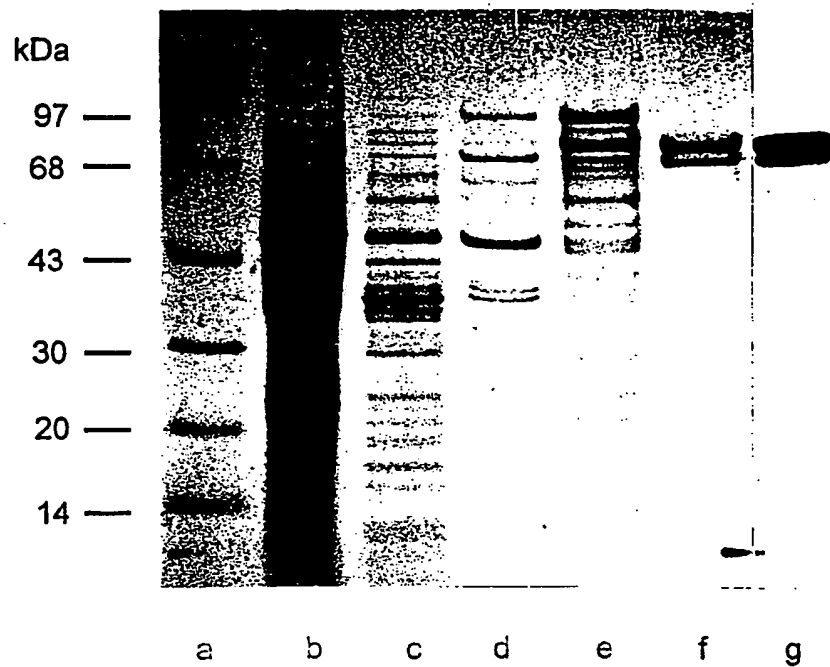


Fig. 3

29 10 No:

26 Mm-FAP
27 Hs-DPP
28 Fm-DPP
29 Pg-DPP
30 PTP-A

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1 MKTPWVVLGLLGAATAVTITVPVV LN GTDD TADS - KTYT - T YLRNT RLKLYS
1 ---MKKKIESLISIAVAFHGLSAQE TLDK YS Q RA - GISGASND-----
1 -MKRPVILLIGINTCAQAOTGNKP DL E TS M YA SAGSGS S PD-----
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Fm-DPP 48 -----GNYAT--EPTGLAKYSYK SQ--KEKN VDG FQGYT-----SNDESK--MI
Pg-DPP 51 -----GNYTE NRERTATRYNYASCKAVD FSVERARECPFKQIQNYE SSTGHHII
56 GLQWMC NY F E---GDD VNKANKSAQ TRFSAADLNALMPEGCK QT DAFPSFR

Mm-FAP 114 DESDYSK RYSYATAT YDLONGEF RGY LPRPIQY C SPVGSKEAYVY NNIIYK
Hs-DPP 116 LEYNYVKQ RHSTAS DIDLNRQ TEERIPNNTQW T SPVGHKEAYVWNE IYK
Fm-DPP 92 LQKSSQS RHSELEK E KDLKSRIV SINNANWIOE PRFSPDCKVAFLADNNEKYQ
Pg-DPP 106 LETDMES RHSYRAAVYDWRNLVKPLS HVGKVMIPTFSPDGRMVAIVRDNNIEYK
113 TLDAGRG VVLFTQ GLVG D LARKVYLE TNEETAS DESPVGD VAYVR ENIYA

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Hs-DPP 176 IEP--NLPSYRITWTG IIFYNG TDWVYEEEVFSAYSALWSENCTFLA AOF EV
Fm-DPP 151 DLN--TGKITQITDG KNEIING GDWVYEEEFHADYYQWN KACDALVEVREDPRKV
166 KFD--F TEVQVITDQINSILNGATDWVYEEEFVTNLMSWS ADNAELAFVRSDES AV
173 RGGKLG GMSRAIAVTI GTETLVYGOAVH REFGIEKGTFS PRGSCLAFYRMOOSAV

Mm-FAP 232 PIHAYSYYG DG--QYPRU NPYPKAGAKNPVVR VDTTYP HVG---P E PVEEMI
Hs-DPP 234 PIHEYSEYSDSLOYPKVR PYPKAGAVNPTVKF V TD LS VTNATS TAPASM
Fm-DPP 208 PEIN PIYYQN--LYPKL TYKYPKAGEENSAV A Y S G AQ-----FGSSEKY
Pg-DPP 223 BEYR PMYEDK--LYPEDIYKYPKAGEKNSTV H Y V ADRN KS-----S PIDADG
232 KPTP VDMHP--LEAE KP YYPMAGTPSHHV G YH A G VY-----TGEPEK

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Fm-DPP 262 IPQ Q N---ANDEE VATANR QNKVD K NTK AAVS-----K FTE DN W
Pg-DPP 277 IPR A D---NADEE AV TLNRLQDFK YY HPK LVPK-----L Q MNKR
285 TN S P---DENI YVAEVNRAONECKVAYDAE GRFVR-----T FVE DKH

Mm-FAP 347 AGGFF TPAFSQDATSY KIFS DG HHH IKDTVENAIQITSCWEATY R TQD
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Fm-DPP 311 TDN --EFLDONS--ELAS DGH HLYYDAAG K QVSKGWEHINY GYNPK
Pg-DPP 326 VSDW QT KEITG G--BAVS DG AHIYLYDNKGV H RITSGNWVTK G DAS
335 VPLHP--TELPGSNNO SI CSR DG NHLYYDTTG I QTKGEWEVTFNAGFDPK

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Fm-DPP 368 ---TKE YIQ TEKGSIN VSK NINTG---KTOLLSNAEGNN AAFSKTFNYE INTS
Pg-DPP 384 ---GT YIQ ABESPIRRAVYA DAKGR---KTSLSLNVGTN DALESNGYAYYINTY
393 ---G R YFE TEASPE RHFYC DIKGG---KTDLTPESGMHRTQLSPD SAIDHIF

Mm-FAP 467 Y PCIPES HDGRTDO QVLEENKEL NSL NI PKVE KK K D GLTF YKMI
Hs-DPP 473 S PCIPY HSSVNDK QVLEDNSAL KML ONV PSKK DFI I LNETKF YOMI
Fm-DPP 421 S TAKYPTKY LKDANGK EL ONDDLLNKU SD FIAKEFITIPNA GDQ NAWMIK
Pg-DPP 435 SSATPA V IFRSKGAK TLEENVALRERL AYRYNPKEFTTIKTQSCLE NAWMIK
446 Q SPY PRKVTVTNIG KGS TLL AKNP TGYAMPE RTGT MAAD---QTP YKMT

Mm-FAP 525 PPQFDRSKKYPILLI QVYEGGCSQS SVKSV AVN---WITYLASKEGI IAVDGRGTAGCG
Hs-DPP 531 PPHFDRSKKYPILLI DVYAGCSQKADIV RLN---WATYLASTENI VASFDGRGSGCG
Fm-DPP 480 PKNFDPK KYPVLFQYSGPSQKQVANS DGGNGIWFDM LAQKG YVVCVDGRGTGARG
Pg-DPP 495 PIDFDPSE YPVLFQYSGPNSQOVLDR SFD---WEHYLASKG YVVCVDGRGTGARG
502 PLHFDPK KYPVLFYVYEGGPHQLVTKT RSSVGGNDIYLAQKG YAVFTVDSRG ANRG

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Fig. 3

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Fm-DPP 539 TRMKKVTYKNLGKYETEDQITAAKWEGNQSIVDKSRIGIEGWSYGGYMASTAMTKGADV
Pg-DPP 551 DEWRCTYMCLGVESDDQIAATAIGOPPVDAAIRIGIWGWSYGGYTILSLCRNGTF
561 AADEQVTHRRLGOTEMADOMCGVDFIKSQSVVDADRIGIEGWSYGGEMTINLMLTHGDVF
*→

Mm-FAP 642 KCGIAPVPVSSWEYYASTYSERFMGLPTRDDNLEHYKNSIVMARAEYFRNVDYLLIHGTA
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Fm-DPP 599 KCGIAPVPVNWREYDSIYTERFLQTPQENK--EGYDLNSPTTYAKLLKG-KELLIHGTA
Pg-DPP 611 KAGIAPVPVADWREYDSYTERFMRTPKENA--SGYKSSAEDVASQLQG-NILIVSCSA
621 KVGVAAGPVIDWNRVETMYGERVFDAPQENP--EGYDAENDEKRAEDLKG-RVMLIHCAI

Mm-FAP 702 DDNVHFQNSAQIAKALVNAQVDFQAMWYSDONHGISSGRSONHLYTHMTHTFKQCFSLSD
Hs-DPP 708 DDNVHFQNSAQISKALVDVGYDFQAMWYDDEHGIASSTAHOHLYTHMTSHFTKQCFSLP-
Fm-DPP 656 DDNVHFQNSMEFSEALQONKKQDFEMAYPDKNHSIIIGGNIRPOLYKMTNMLLEN-----
Pg-DPP 668 DDNVHLQNTMLFTEALVQANTPEDMAIYMDKNHSIIYGGNIRVHLYTRAKFFPDNL-----
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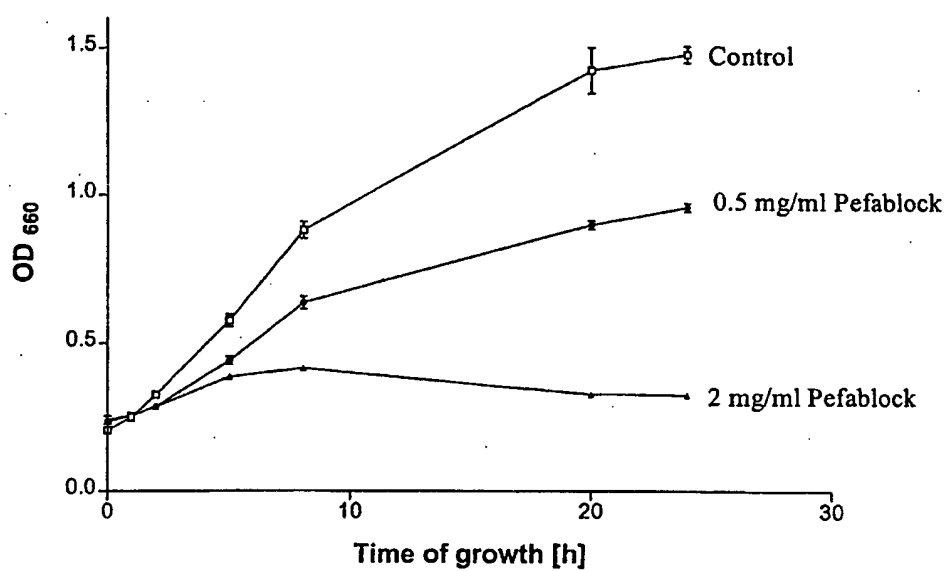
Fig. 4

See ID No:

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350	VDADRIGVHGWSYGGYAT	PLEVQCGANDPRVNI	ESDQIVTALRARGFEVP	YVWYKNECHGF	YHRENS	524
640	VNGKVKCGEGASYGGFMT	PLLTTHGSDVNNVPTAES	VMLYNALKILGREVER	FEETEDQDHF	FEPEPERR	810
495	VDGDRIGAVGASYGGFSV	PILLTHGSDTFLASQ	WAAFTAAQLRGVPS	WMLP	PDENHWAQ	667

Fig 5

Influence of Pefablock- serine proteinase inhibitor on *P. gingivalis* growth.



Seq ID No:

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 4287PP 1 -----VPDGEHY--TEMNRERT
 4365PP 1 -----VDKGG--NENYHLFA
 44101PP 1 MKKSLMLLSAATLSSIEAQTIOQMKAGGPWPVRAAKTDTVGMNGSKYNPADLLRQAY
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126PP 55 VGLQWMGDNYVF---IEGDDLANKANG-----KSAQTTRESAADLNALMPEGCKEQ
 87PP 16 AILRY--SYAS---GKAVDTUSVER-----ARECPKQIQ-N-----YE
 65PP 14 SNIDG---S---NTRDLTPEDGVK---ASILNMLKEQK-D-----YM
 101PP 61 DATDKDLRNVSAADKDGRIAGRKAGSKAERSEMAVYSFALTAEHAKADIEVFGQGRMSLW
 9PP 57 AVSFP--DVKT-----NKATRELTVNLD-----GSGRKQITDTESN-----EYAPAW

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 65PP 46 TISMNK---NNPO---IFEPYKLNVTETLTQLYEN---KDAANPTQGYEFDK---
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 9PP 144 -E-----E-KVLELTND-----IKFGRKTKDITVPDLDK

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 65PP 112 -LATGEFRELKK--THDDTFGVIAFNIA-----SKN-KDPAVVLNLD---S
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 65PP 224 GKE--FSVV---S---YCD-
 101PP 421 GKH--LIVGGS-ALAFGNIGNLKSGVTNSYDKQFFLFDLSIRKATALTKNENPSVSAG
 9PP 287 GKS--IATISMERDGYES-----DLKRLFVADLAIGKRTHVNPTFDYNVDMI

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 65PP 235 -EE--I-LLIAVSDKLYGTYYQFETG--PK-----KFT-----LTYD-L
 101PP 478 RECRKNN-YTFRAENG-SRKQYRLKLTLEISOETGEDVVQWFGVAADNGAVWYSGQ
 9PP 332 QVAPDSKGYELACKEA--ETNLWEITLKTGNIROITQGDHYADFSVRND---VMLAKR

Fig. 6

Fig. 6

```

126PP 446 QSPVIRKVTITNIGKSHITLLEAKNPDTGYAPETPTG-----TIMAADGQTPLYKLT
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65PP 269 -----HQLK-----EEF-----MAETRPI-----KFKSRDG-LTIHGFTT
101PP 536 SENNADRLYRFDGTSGKLVDLSAEKLANIDFTPAROWN-----YTAPOG-TVVEGYY
9PP 387 HSELEDDLYRVNLNNGAAQAVTAEKVVILRLTPTTCEKR---WKTTDG-GNMLTAVV

126PP 501 MELHFDPAKKYEVIVVYGG---EHALVTKTWRSVGGWDIYMAQKGYAVFTVDSRGSAN
87PP 447 KEIDFDSRHYFVLNVQYSG---ENSDQVLD--RYSFD-WEHYLASKGYVAVDGRGTGA
65PP 299 LKAALECKKVFLLVNFHSG---E---GIRD--SWGPNPETOLFASRGYATLOVNFRISSG
101PP 589 LEPQDFDSKKYFMLVYYGGTSEINRTLEG--HYSLA---MYAACSYVVYTLNPSITTS
9PP 443 LEPNFDKKNKYFALLYCQSG---E---NTVS-QFWSHRWNLRLMAEQSYIVIAPNRHGVPG

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65PP 353 YGKEELRAGFKQLGRKAMDEVEDGVR-VAISQGNVLEDRITAIYGASLGGYATLMGLVKTTP
101PP 643 YGQELYAARHVNAWSDRTADEILGATKEFIRTHSEVNGKKVQCFGASVGGFMTQYIQTNT-
9PP 498 FGQKNEQISGDYEGQNRDYLTAVD-EMKKEPVLDGRICAVGASVGGFSVYWLAGHHD

126PP 618 DVEKVGAVAGSPVI-----D-----NN--RYEIMYGERYFDA--EQENPEGYD-AANLLK
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101PP 702 EIFAAAVSHAGISSIS---N---YNGSGYNGGISTVASTDSYPWNPPDLHAGHSELFRR
9PP 557 KRFAAFLAHAGIFN-EMQYATTEEMFA-NNDIGGFWEKLN---VVAQRTYA-TSPHKF

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65PP 469 ID-KINKPLEVVQSANPRNINIESDQIVTALRAREFEVPMVKYNEGIGFHRENSMEL
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9PP 612 VQ-NWDTTILMIHGELIFRILASQAMAAFDAAQLRQVPSEMLIYPDENWVLOEQNALLF

126PP 721 YETITRYFTDHI-----
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```

Fig 7

P. gingivalis W 83 PTP sequence

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 13768 atgtcacgagctatcgctgtgactatcgatggaactgagactctc
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 V Y G Q A V H Q R E F G I E K
 13858 ggtacattctggtctccaaaaggagctgccttgctttctatcga
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 13948 ccgctcgaagccgagtcctaaacggctttattaccccatggcagg
 P L E A E S K P L Y Y P M A G
 13993 actccgtcacaccacgttacgggtgggatctatcatctggccaca
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 G K T V Y L Q T G E P K E K F
 14083 ctgacgaatttgagttggagtccggacgaaaatatcttgatgta
 L T N L S W S P D E N I L Y V
 14128 gctgaggtgaatcgctcctcaaaacgaatgtaaggtaaatgcctat
 A E V N R A Q N E C K V N A Y
 14173 gacgctgagaccggtagattcgctccgtacgctttttgttgaaacc
 D A E T G R F V R T L F V E T

Fig. 7

14218 gataaacattatgtagagccgttacatcccctgacattccttcog
D K H Y V E P L H P L T F L P
14263 ggaagtaacaatcagttcatttggcagagccgtcgcgacggatgg
G S N N Q F I W Q S R R D G W
14308 aaccatctctatctgtatgatactacaggtcgtctgatccgtcag
N H L Y L Y D T T G R L I R Q
14353 gtgacaaaaggggagtgagggttacaaactttgcaggcttcgat
V T K G E W E V T N F A G F D
14398 cccaaggaacacggctctatttcgaaagtaccgaagccagccct
P K G T R L Y F E S T E A S P
14443 ctcgaaacgccatttttactgtattgatataaaaggaggaaagaca
L E R H F Y C I D I K G G K T
14488 aaagatctgactccggagtcgggaatgcaccgcactcagctatct
K D L T P E S G M H R T Q L S
14533 cctgatgggttctgccataatcgatatttttcagtcacctactgtc
P D G S A I I D I F Q S P T V
14578 ccgcgtaaggttacagtgacaaatatcggcaaaggggtctcacaca
P R K V T V T N I G K G S H T
14623 ctcttgagggttaagaaccccgatacgggctatgccatgccggag
L L E A K N P D T G Y A M P E
14668 atcagaacgggtaccatcatggcgccgatgggcagacacctctt
I R T G T I M A A D G Q T P L
14713 tattacaagctcacgatgccgcttcatttcgatccggcaaagaaa
Y Y K L T M P L H F D P A K K
14758 tatcctgttattgtctatgtttacggaggacctcatgcccaactc
Y P V I V Y V Y G G P H A Q L
14803 gtaaccaagacatggcgagctctgtcgggtggatgggatattctat
V T K T W R S S V G G W D I Y
14848 atggcacagaaaggctatgccgtctttacgggtggatagtcgcgga
M A Q K G Y A V F T V D S R G
14893 tctgccaatagaggggctgcttttcgagcagggttattcatcgtcgt
S A N R G A A F E Q V I H R R
14938 ttggggcagaccgagatggccgatcagatgtgcggtgtggatttc
L G Q T E M A D Q M C G V D F
14983 ctcaagagccaatcatgggtggatgccgatagaataggagtagat
L K S Q S W V D A D R I G V H
15028 ggctggagctatgggtggctttatgactacgaatctgatgcttacg
G W S Y G G F M T T N L M L T
15073 cacggcgatgtcttcaaagtcggagtagccggcgggcctgtcata
H G D V F K V G V A G G P V I
15118 gactggaatcgatatgagattatgtacggtgagcgttatttcgat
D W N R Y E I M Y G E R Y F D
15163 gcgccacaggaaaatcccgaaggatacgtatgctgccaacctgtc
A P Q E N P E G Y D A A N L L
15208 aaacgagccggtgatctgaaaggacgacttatgctgattcatgga
K R A G D L K G R L M L I H G
15253 gcgatcgatccggtcgtggtatggcagcattcactccttttcctt

Fig 7

A I D P V V V W Q H S L L F L
 15298 gatgcttgctgaaggcacgcacctatcctgactattacgtctat
 D A C V K A R T Y P D Y Y V Y
 15343 ccgagccacgaacataatgtgatggggccggacagagtacatttg
 P S H E H N V M G P D R V H L
 15388 tatgaaacaataacccgttatttcacagatcacttatga 15426
 Y E T I T R Y F T D H L *

SEQ ID NO: 38
 TCAGTCTCCTGAAACGAGTGGTAAGGAGTTTACTCTTGAGCAACTGATGCCCGAGGAAAAGAGTTTATA
 ACTTTTACCCCGAATACGTGGTTCGGTTTGCAATGGATGGGAGACAATTATGTCTTTATCGAGGGTGATGAT
 TTAGTTTTTAATAAGGCGAATGGCAATCGGCTCAGACGACCAGATTTTCTGCTGCCGATCTCAATGCACT
 CATGCCGGAGGGATGCAATTTTCAGACGACTGATGCTTCCCTTCATTCCGCACACTCGATGCCGGACGGG
 GACTGGTCTGTTCTATTTACCCAAGGAGGATTAGTCGGATTTCGATATGCTTGCTCGAAAAGGTGACTTATCTT
 TTCGATACCAATGAGGAGACGGCTTCTTTGGATTTTCTCCTGTGGGAGACCGTGTGCCTATGTCAGAAA
 CCATAACCTTTACATTGCTCGTGGAGGTAAATGGGAGAAGGTATGTCACGAGCTATCGCTGTGACTATCG
 ATGGAACGAGACTCTCGTATATGGCCAGGCCGTACACCAGCGTGAATTCGGTATCGAAAAAGGTACATTC
 TGGTCTCCAAAAGGGAGCTGCCTTGCTTTCTATCGAATGGATCAGAGTATGGTGAAGCCTACCCCGATAGT
 GGATTATCATCCGCTCGAAGCCGAGTCCAAACCGCTTATTACCCCATGGCAGGTACTCCGTCACACCAG
 TTACGGTTGGGATCTATCATCTGGCCACAGGTAAGACCGTCTATCTACAAACGGGTGAACCCAAGGAAAA
 TTTCTGACGAATTTGAGTTGGAGTCCGGACGAAAATATCTGTATGTAGCTGAGGTGAATCGTCTCAAAA
 CGAATGTAAGGTAAATGCCTATGACGCTGAGACCGGTAGATTGCTCCGTACGCTTTTGTGTAACCGATA
 AACATTATGTAGAGCCGTACATCCCTGACATTCTTCCGGGAAGTAACAATCAGTTCATTGTGGCAGAGC
 CGTCGCGACGGATGGAACCATCTCTATCTGTATGATACTACAGGTCTGCTGATCCGTCAGGTGACAAAAG
 GGAGTGGGAGGTTACAACTTTGCAGGCTTCGATCCCAAGGGAACACGGCTCTATTTCGAAAGTACCGAAG
 CCAGCCCTCTCGAACGCCATTTTACTGTATTGATATCAAAGGAGGAAGACAAAAGATCTGACTCCGGAG
 TCGGGAATGCACCGCACTCAGCTATCTCCTGATGGTTCTGCCATAATCGATATTTTTCAGTCACCTACTGT
 CCCGCGTAAGGTTACAGTGACAAATATCGGCAAAGGGTCTCACACACTCTTGGAGGCTAAGAACCCCGATA
 CGGGCTATGCCATGCCGGAGATCAGAACGGGTACCATCATGGCGGCCGATGGGCAGACACCTCTTTATTAC
 AAGCTCACGATGCCGCTTCATTTCGATCCGGCAAAGAAATATCCTGTTATTGTCTATGTTTACGGAGGACC
 TCATGCCCAACTCGTAACCAAGACATGGCGCAGCTCTGTCCGTGGATGGGATATCTATATGGCACAGAAAG
 GCTATGCCGCTCTTACGGTGGATAGTCCGGATCTGCCAATAGAGGGGCTGCTTTCGAGCAGGTATTTCAT
 CGTCGTTTGGGGCAGACCGAGATGGCCGATCAGATGTGCGGTGTGGATTTCCTCAGAGCCAATCATGGGT
 GGATGCCGATAGAATAGGAGTACATGGCTGGAGCTATGGTGGCTTTATGACTACGAATCTGATGCTTACGC
 ACGGCGATGTCTTCAAAGTCGGAGTAGCCGCGGGCTGTCTAGACTGGAATCGATATGAGATTATGTAC
 GGTGAGCGTTATTTTCGATGCCGCCACAGGAAATCCCGAAGGATACGATGCTGCCAACCTGCTCAAACGAGC
 CGGTGATCTGAAAGGACGACTTATGCTGATTCATGGAGCGATCGATCCGGTCTGGGTATGGCAGCATTCAC
 TCCTTTTCTTGTATGCTTGCGTGAAGGCACGCACCTATCCTGACTATTACGTCTATCCGAGCCACGAACAT
 AATGTGATGGGGCCGGACAGAGTACATTTGTATGAAACAATAACCCGTATTTTCACAGATCAGTTATGA



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- (54) Title: BACTERIAL PROLYL PEPTIDASES AND METHODS OF USE**

[illegible]

(57) Abstract: The present invention provides isolated polypeptides, prolyl tripeptidyl-peptidases, and active analogs, active fragments or active modifications thereof, having amidolytic activity for cleavage of a peptide bond present in a target peptide having at least 30 amino acids. Isolated nucleic acid fragments encoding isolated prolyl tripeptidyl-peptidases are also provided, as are methods of reducing growth of a bacterium by inhibiting a prolyl tripeptidyl-peptidase.

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BACTERIAL PROLYL PEPTIDASES AND METHODS OF USE

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CONTINUING APPLICATION DATA

This patent application claims the benefit of U.S. provisional patent application No. 60/123,148, filed March 5, 1999, which is incorporated by reference herein.

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BACKGROUND OF THE INVENTION

Porphyromonas gingivalis (formerly *Bacteroides gingivalis*) is an obligately anaerobic bacterium which is implicated in periodontal disease. *P. gingivalis* produces several distinct proteolytic enzymes, many of which are recognized as important virulence factors. A number of physiologically significant proteins, including collagen, fibronectin, immunoglobulins, complement factors C3, C4, C5, and B, lysozyme, iron-binding proteins, plasma proteinase inhibitors, fibrin and fibrinogen, and factors of the plasma coagulation cascade system, are hydrolyzed by *P. gingivalis* proteases. Broad proteolytic activity plays a role in the evasion of host defense mechanisms and the destruction of gingival connective tissue in progressive periodontitis.

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Progressive periodontitis is characterized by acute tissue degradation promoted by collagen digestion and a vigorous inflammatory response characterized by excessive neutrophil infiltration. Gingival crevicular fluid accumulates in periodontitis as periodontal tissue erosion progresses at the foci of the infection, and numerous plasma proteins are exposed to proteinases expressed by the bacteria at the injury site. Neutrophils are recruited to the gingiva, in part, by the humoral chemotactic factor C5a. The complement components C3 and C5 are activated by complex plasma proteases with "trypsin-like" specificities called convertases. The human plasma convertases

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cleave the α -chains of C3 and C5 at a specific site generating biologically active factors known as anaphylatoxins (i.e. C3a and C5a). The anaphylatoxins are potent proinflammatory factors exhibiting chemotactic and/or spasmogenic activities as well as promoting increased vascular permeability. The larger products from C3 and C5 cleavage (i.e. C3b and C5b) participate in functions including complement cascade activation, opsonization, and lytic complex formation.

Recent studies have indicated that this periodontopathogen produces at least seven different enzymes belonging to the cysteine and serine catalytic classes of peptidases, among which three cysteine proteinases (gingipains) are predominant (Potempa, J., et al. (1995) *Prospect. Drug Discovery and Design* 2, 445-458). The gingipains are the best characterized group of *P. gingivalis* enzymes as their structure, function, enzymatic properties and pathological significance are known. From *in vitro* studies it is apparent that two gingipains R (also referred to generally as "Arg-gingipains" and more specifically as RgpA and RgpB), enzymes specific for cleavage at Arg-Xaa peptide bonds, have a significant potential to contribute to the development and/or maintenance of a pathological inflammatory state in infected periodontal pockets through: (i) activation of the kallikrein-kinin cascade, (ii) the release of neutrophil chemotactic activity from native and oxidized C5 of the complement pathway, and (iii) activation of factor X. In addition, gingipain K (also referred to as "Lys-gingipain"), an enzyme which cleaves Lys-Xaa peptide bonds, degrades fibrinogen. This may add to a bleeding on probing tendency associated with periodontitis. Finally, the presence of a hemagglutinin/adhesion domain in the non covalent multiprotein complexes of RgpA and gingipain K suggests participation of these enzymes in the binding of *P. gingivalis* to extracellular matrix proteins which may facilitate tissue invasion by this pathogen.

In comparison to the gingipains, relatively little is known about other cysteine proteinases produced by *P. gingivalis*. Two genes, referred to as *tp* and *prtT* have been cloned and sequenced and although they encode a putative papain-like and streptopain-like cysteine proteinases, respectively, neither has been purified and characterized.

The presence of serine proteinase activity in cultures of *P. gingivalis* has been known for several years; however, only limited information is available about such enzymes. Indeed, a serine endopeptidase has been isolated from culture media, although it was only superficially characterized (Hinode D., et al.,
5 (1993) *Infect. Immun.* 59, 3060-3068). On the other hand, an enzyme referred to as glycylprolyl peptidase (DPP IV) was found to be associated with bacterial surfaces and two molecular mass forms of this peptidase have been described. This enzyme has also been shown to possess the ability to hydrolyze partially degraded type I collagen, releasing the Gly-Pro dipeptide, and it was suggested
10 that, in collaboration with collagenase, glycylprolyl peptidase may contribute to the destruction of the periodontal ligament (Abiko, Y., et al. (1985) *J.Dent. Res.* 64, 106-111). In addition to this potential pathological function, glycylprolyl peptidase may also play a vital role in providing *P. gingivalis* with dipeptides which can be transported inside the cell and serve as a source of carbon,
15 nitrogen, and energy for this asaccharolytic organism. Recently, a gene encoding glycylprolyl peptidase in *P. gingivalis* has been cloned and sequenced, and it is now apparent that this enzyme is homologous to dipeptidyl-peptidase IV (DPP-IV) from other organisms (Kiyama, M., et al. (1998) 1396, 39-46). The nucleotide sequence of the genome of this bacterium is currently being
20 determined by The Institute for Genomic Research, and is available at www.tigr.org.

SUMMARY OF THE INVENTION

The present invention is directed to an isolated prolyl tripeptidyl-
25 peptidase, active analog, active fragment, or active modification thereof having amidolytic activity for cleavage of a peptide bond present in a target polypeptide having at least 4 amino acids. Alternatively, the isolated prolyl tripeptidyl-peptidase, active analog, active fragment, or active modification thereof is isolated from *P. gingivalis*. Typically, amidolytic activity is determined with a
30 prolyl tripeptidyl-peptidase:target polypeptide ratio of at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours. The peptide cleaved by the isolated prolyl tripeptidyl-peptidase can include the sequence of SEQ ID NO:1, SEQ ID NO:2, SEQ ID

NO:7, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:11, H-Ala-Arg-Pro-Ala-D-Lys-amide, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:25, or SEQ ID NO:37. The amino acid sequence of the isolated prolyl tripeptidyl-peptidase can include the amino acid sequence GXSTXXG (SEQ ID NO:39), the amino acid sequence GXSTXGG (SEQ ID NO:40), or the amino acid sequence of SEQ ID NO:30.

Another aspect of the invention is an isolated polypeptide, active analog, active fragment, or active modification thereof having amidolytic activity for cleavage of a peptide bond present in a target polypeptide having at least 4 amino acids. Typically, the polypeptide:target polypeptide ratio of at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours.

The invention is also directed to an isolated polypeptide comprising an amino acid sequence having a percentage amino acid identity of greater than 35 % with SEQ ID NO:30.

An alternative aspect of the invention is an isolated nucleic acid fragment encoding a prolyl-tripeptidyl peptidase, active analog, active fragment, or active modification thereof, having amidolytic activity for cleavage of a peptide bond present in a target polypeptide having at least 4 amino acids. Typically, the prolyl tripeptidyl-peptidase:target polypeptide ratio of at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours. The nucleic acid fragment can have a nucleotide sequence comprising SEQ ID NO:38. A complement of the nucleic acid fragment can hybridize to SEQ ID NO:38 under hybridization conditions of 0.5 M phosphate buffer, pH 7.2, 7 % SDS, 10 mM EDTA, at 68°C, followed by three for 20 minutes washes in 2x SSC, and 0.1 % SDS, at 65°C, wherein at least about 20 nucleotides of the complement hybridize.

Another aspect of the invention is an isolated nucleic acid fragment encoding a polypeptide that includes an amino acid sequence having a percentage amino acid identity of greater than 35 % with SEQ ID NO:30.

The invention is also directed at a method of identifying an inhibitor of a prolyl-tripeptidyl peptidase, active analog, active fragment, or active modification thereof, including identifying a molecule that inhibits the

amidolytic activity of the prolyl-tripeptidyl peptidase. The inhibitor is identified by incubating the prolyl-tripeptidyl peptidase with the molecule under conditions that promote amidolytic activity of the prolyl-tripeptidyl peptidase and determining if the amidolytic activity of the prolyl-tripeptidyl peptidase is inhibited relative to the amidolytic activity in the absence of molecule.

An aspect of the invention is a method of reducing growth of a bacterium. This method includes inhibiting a prolyl tripeptidyl-peptidase, active analog, active fragment, or active modification thereof, or a prolyl dipeptidyl-peptidase, active analog, active fragment, or active modification thereof. The method includes contacting the prolyl tripeptidyl-peptidase with an inhibitor of the prolyl tripeptidyl-peptidase. The method can be used to protect an animal from a periodontal disease caused by *P. gingivalis* including administering to the animal the inhibitor. The disease can be selected from the group consisting of gingivitis and periodontitis. The inhibitor can be administered by a method selected from the group consisting of subgingival application and controlled release delivery.

Another aspect of the invention is an immunogenic composition including an isolated prolyl tripeptidyl-peptidase, or an antigenic analog, antigenic fragment, or antigenic modification thereof, the prolyl tripeptidyl-peptidase having amidolytic activity for cleavage of a peptide bond present in a target peptide having at least 4 amino acids. Typically, the prolyl tripeptidyl-peptidase:target polypeptide ratio is at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours. The immunogenic composition can include an adjuvant.

The invention is also directed to a composition including an inhibitor of an isolated prolyl tripeptidyl-peptidase and a pharmaceutically acceptable carrier.

Additional aspects of the invention include a dipeptidyl peptidase having an amino acid sequence including SEQ ID NO:43, SEQ ID NO:44, or SEQ ID NO:45.

Definitions

“Polypeptide” as used herein refers to a polymer of amino acids and does not refer to a specific length of a polymer of amino acids. Thus, for example, the terms peptide, oligopeptide, protein, and enzyme are included within the definition of polypeptide. This term also includes post-expression modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations, and the like. A polypeptide can be produced by an organism, or produced using recombinant techniques, or chemically or enzymatically synthesized.

“Peptidase,” “proteinase,” and “protease” all refer to enzymes that catalyze the hydrolysis of peptide bonds in a polypeptide. A “peptide bond” or “amide bond” is a covalent bond between the alpha-amino group of one amino acid and the alpha-carboxyl group of another amino acid. “Peptidase inhibitor,” “proteinase inhibitor,” “protease inhibitor,” and “inhibitor” all refer to molecules that inhibit a peptidase that catalyzes the hydrolysis of peptide bonds in a polypeptide.

As used herein, the term “isolated” means that a polypeptide or a nucleic acid fragment has been either removed from its natural environment, produced using recombinant techniques, or chemically or enzymatically synthesized. Preferably, the polypeptide or nucleic acid fragment is purified, i.e., essentially free from any other polypeptides or nucleic acid fragments and associated cellular products or other impurities.

“Amidolytic activity” refers to the ability of a polypeptide to catalyze the hydrolysis of at least one peptide bond in a polypeptide. The term “cleavage” can also be used to refer to the hydrolysis of a peptide bond in a polypeptide.

“Prolyl-tripeptidyl peptidase” and “PTP” refer to a polypeptide having a particular “amidolytic activity”. A “prolyl-tripeptidyl peptidase” is able to hydrolyze the peptide bond between the proline and the Yaa residues in a target polypeptide with the general formula $\text{NH}_2\text{-Xaa-Xaa-Pro-Yaa-(Xaa)}_n$ (SEQ ID NO:25), wherein Xaa is a natural or modified amino acid, Yaa is a natural or modified amino acid except proline, and the α -amino of the amino terminal residue is not blocked. A “prolyl tripeptidyl-peptidase” does not have to cleave all members of the target peptide. The term “natural amino acid” refers to the 20 amino acids typically produced by a cell. The term “modified amino acid”

refers to, for instance, acetylation, hydroxylation, methylation, amidation, and the attachment of carbohydrate or lipid moieties, cofactors, and the like.

A “target polypeptide” is a polypeptide that is the potential substrate of the amidolytic activity of a prolyl tripeptidyl-peptidase.

5 An active analog, active fragment, or active modification of a polypeptide of the invention is one that has amidolytic activity by hydrolysis of a peptide bond present in the target polypeptide as described herein. Active analogs, fragments, and modifications are described in greater detail herein.

10 “Nucleic acid fragment” as used herein refers to a linear polymeric form of nucleotides of any length, either ribonucleotides or deoxynucleotides, and includes both double- and single-stranded DNA and RNA. A nucleic acid fragment may include both coding and non-coding regions that can be obtained directly from a natural source (e.g., a microorganism), or can be prepared with the aid of recombinant or synthetic techniques. A nucleic acid molecule may be
15 equivalent to this nucleic acid fragment or it can include this fragment in addition to one or more other nucleotides or polynucleotides. For example, the nucleic acid molecule of the invention can be a vector, such as an expression of cloning vector.

20 “Percentage amino acid identity” refers to a comparison of the amino acids of two polypeptides as described herein.

BRIEF DESCRIPTION OF THE FIGURES

25 **Fig. 1. Purification of the prolyl tripeptidyl peptidase from the acetone precipitate of the *P. gingivalis* cell extracts. Absorbance at 280 nm (open triangles), amidolytic activity against H-Ala-Phe-Pro-pNA (closed diamonds), and H-Gly-Pro-pNA (closed circles). (a) Separation of PTP-A on hydroxyapatite. (b) Separation of PTP-A on Phenyl-Sepharose HP. (c) Separation of PTP-A on MonoQ FPLC. (d) Chromatofocusing of PTP-A on Mono-P.**

30 **Fig. 2. SDS -PAGE of fractions from purification of PTP-A and the autoradiography of the purified enzyme. Lane a, molecular mass markers (phosphorylase B, 97 kDa; bovine serum albumin, 68 kDa; ovalbumin, 43 kDa; carbonic anhydrase, 30 kDa; soybean trypsin inhibitor, 20 kDa; α -lactalbumin, 14**

kDa); *lane b*, acetone precipitate from Triton X-100 extract of *P. gingivalis*, *lane c*: hydroxyapatite column eluate; *lane d*, Phenyl-Sepharose column eluate; *lane e*, MonoQ column eluate; *lane f*, purified PTP-A from MonoP column wash; *lane g*, autoradiograph of ^3H -DFP labeled enzyme exposed for 96 h to X-ray film. All samples were reduced and boiled prior to PAGE analysis.

Fig. 3. Multiple sequence alignment of *P. gingivalis* PTP-A (PTP-A) and its bacterial and eukaryotic homologues. Pg-DPP, DPP from *P. gingivalis* (Kiyama, M., et al., (1998) *Bioch. Bioph. Acta* 1396, 39-46) containing an amino-terminal sequence corrected according to the *P. gingivalis* W83 genome data available from The Institute of Genomic Research at www.tigr.org); Fm-DPP, DPP from *Flavobacterium meningosepticum*; Hs-DPP, human DPP IV; and Mm-FAP, mouse fibroblast activation protein. Peptide sequences obtained from PTP-A analysis described herein are indicated with arrows (note that the sequence of the peptide 81-97 corresponds to the N-terminus of the lower molecular weight form of PTP-A); catalytic triad is marked with asterisks; and the proposed PTP-A membrane-anchoring N-terminal α -helix is double-underlined. Homologous regions (i.e., regions of identical amino acids and/or conservative substitutions) are highlighted. Identical regions are shown as white letters on a black background.

Fig. 4. Comparison of *P. gingivalis* PTP-A and DPP active site domains to corresponding sequences of three putative homologues identified within the *P. gingivalis* genome (DPP-H1, DPP-H2 and DPP-H3). Sequences of *P. gingivalis* PTP-A, DPP, DPP-H1, DPP-H2, and DPP-H3 were obtained from conceptual translation of the following open reading frames retrieved from The Institute for Genomic Research (TIGR) unfinished *P. gingivalis* genome database: gnl | TIGR | *P. gingivalis* contig 126 (positions 13 228 – 15 426), contig 87 (positions 6 424 – 4 399), contig 65 (positions 161 – 1 786), contig 101 (positions 8 895 – 6 845), and contig 9 (positions 4 216 – 2 162), respectively. Residues predicted as catalytic triads are marked with asterisks. Homologous regions (i.e., regions of identical amino acids and/or conservative substitutions) are highlighted.

Identical regions are shown as white letters on a black background. Similar regions (i.e., conservative substitutions) are shown as white letters on a grey background.

5 **Fig. 5. Influence of Pefabloc-serine proteinase inhibitor on *P. gingivalis* growth.**

Fig. 6. Comparison of *P. gingivalis* PTP-A and DPP to sequences of three putative homologues identified within the *P. gingivalis* genome (DPP-H1, DPP-H2 and DPP-H3). Sequences of *P. gingivalis* PTP-A (126PP), DPP (87PP),
10 DPP-H1 (65PP), DPP-H2 (101PP), and DPP-H3 (9PP) were obtained as described in Fig. 4. Homologous regions (i.e., regions of identical amino acids and/or conservative substitutions) are highlighted. Identical regions are shown as white letters on a black background. Similar regions (i.e., conservative substitutions) are shown as white letters on a grey background.

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Fig. 7. Nucleotide sequence (SEQ ID NO:38) and amino acid sequence (SEQ ID NO:30) of PTP-A.

DETAILED DESCRIPTION OF THE INVENTION

20 The present invention provides isolated polypeptides, preferably isolated prolyl peptidases, more preferably prolyl dipeptidyl-peptidases and prolyl tripeptidyl-peptidases, most preferably prolyl-tripeptidyl peptidases, that have amidolytic activity by hydrolysis of a peptide bond present in a target polypeptide, where the bond is between a proline and an amino acid residue attached to the
25 alpha-carboxyl group end of the proline.

When the prolyl peptidase is a prolyl tripeptidyl-peptidase, the peptidase has amidolytic activity by hydrolysis of a peptide bond present in a target polypeptide of the general formula $\text{NH}_2\text{-Xaa-Xaa-Pro-Yaa-(Xaa)}_n$ (SEQ ID NO:25), wherein Xaa is a natural or modified amino acid, Yaa is a natural or
30 modified amino acid except proline, and the α -amino of the amino terminal residue is not blocked, wherein the peptide bond of the target polypeptide that is hydrolyzed is the Pro-Yaa peptide bond. Preferably, isolated polypeptides do not cleave a target peptide having a blocked α -amino of the amino terminal residue.

Preferably, the only peptide bond of the target peptide that is hydrolyzed is the Pro-Yaa bond. In increasing order of preference, isolated polypeptides can cleave a target peptide that is at least 4 amino acids or at least 300 Da, at least 10 amino acids or at least 750 Da, at least 20 amino acids or at least 1,500 Da, or at least 30 amino acids or at least 3,000 Da. Preferably, the prolyl-tripeptidyl peptidases cleave peptides 1, 2, 7, 8, and 10-15 shown in Table 3, human cystatin C, and interleukin 6.

When the prolyl peptidase is a prolyl dipeptidyl-peptidase, the peptidase has amidolytic activity by hydrolysis of a peptide bond present in a target polypeptide of the general formula $\text{NH}_2\text{-Xaa-Zaa-Yaa-(Xaa)}_n$ (SEQ ID NO:12), wherein Xaa is a natural or modified amino acid, Zaa is a proline or alanine, Yaa is a natural or modified amino acid except proline or hydroxyproline, and the α -amino of the amino terminal residue is not blocked, wherein the peptide bond of the target polypeptide that is hydrolyzed is the Zaa-Yaa peptide bond. Preferably, isolated polypeptides does not cleave a target peptide having a blocked α -amino of the amino terminal residue. Preferably, the only peptide bond of the target peptide that is hydrolyzed is the Pro-Yaa bond.

Due to their cyclic aliphatic character proline residues bestow unique conformational constraints on polypeptide chain structures, significantly affecting the susceptibility of proximal peptide bonds to proteolytic cleavage. Those proline residues, which often appear near the amino-termini of many biologically active peptides, may protect them against proteolytic degradation by peptidases with general specificity. A specialized group of proteolytic enzymes, typically referred to as prolyl peptidases, has evolved to cleave (i.e., hydrolyze) a peptide bond adjacent to a proline residue in a polypeptide. The peptide bond adjacent to a proline residue can be referred to as a prolyl-X bond, where prolyl is the proline residue, and X is an amino acid residue attached to the alpha-carboxyl group end of the proline. The bacterial prolyl peptidases can cleave a polypeptide to liberate a tripeptide or a dipeptide. Prolyl peptidases that do not cleave a target peptide if the α -amino of the amino terminal residue is blocked can be referred to as exopeptidases. The *in vivo* activity of these specialized proteolytic enzymes may have important physiological significance, because it may lead to inactivation of many biologically active peptides and/or transformation of the activity of other

biologically active peptides. In addition, hydrolysis of prolyl-X bonds in conjunction with general catabolic pathways should allow the complete re-utilization of amino acids by living organisms, including bacteria. However, prolyl peptidases from bacterial pathogens, if released into the host environment, may interfere with the physiological functions of biologically active polypeptides and, therefore, contribute to the pathogenicity of infectious disease.

The external (i.e., cell surface) localization and uncontrolled activity of bacterial peptidases, including prolyl peptidases, likely contributes significantly to run-away inflammation in the human host and the pathological degradation of connective tissue during periodontitis. For instance, working in concert bacterial prolyl peptidases (e.g., prolyl tripeptidyl peptidases and DPP IV) have the ability to completely degrade collagen fragments locally generated by endogenous or bacterial collagenases. Because type I collagen is the major component of periodontal ligament, its enhanced degradation by bacterial prolyl peptidases may contribute to loss of tooth attachment and periodontal pocket formation. Thus, there is a need in the art to characterize bacterial peptidases to facilitate the development of therapies to inhibit the activity of the bacterial peptidases.

The polypeptides of the present invention, preferably prolyl peptidases, can be used as a source of antibodies for inhibiting the peptidase activity and thereby possibly reducing periodontitis, loss of tooth attachment and periodontal pocket formation. Antibodies to prolyl peptidases can also be used to identify and/or isolate additional prolyl peptidases. Knowledge of prolyl peptidases can also be used to make inhibitors of prolyl peptidases and to make immunogenic compositions that could be used to elicit the production of antibodies to prolyl peptidases and thereby possibly reduce gingivitis, periodontitis, loss of tooth attachment, and/or periodontal pocket formation.

An example of a prolyl-tripeptidyl peptidase is prolyl-tripeptidyl peptidase A (SEQ ID NO:30) (also referred to as PTP-A) from *P. gingivalis*. Purified PTP-A has apparent molecular masses of 81.8 and 75.8 kDa. The lower molecular mass peptidase may be due to the proteolytic cleavage of the peptidase from the surface of *P. gingivalis*. PTP-A is a new member of clan SC, family S9 of serine peptidases. Clans of serine peptidases are grouped on the basis of the order of certain amino acids in the polypeptide that make up the "catalytic triad" which

plays a pivotal role peptidase activity. The members of the clan SC are characterized by the catalytic triad in the polypeptide in the order of serine, aspartic acid, and histidine. Members of the clan SC are also characterized by a tertiary structure including $\beta/\alpha/\beta$ units, and an α/β hydrolase fold. In addition to the catalytic triad order, the amino acid sequence GX β XXG (SEQ ID NO:39), where X is any amino acid and S is the active site serine, is a signature of all members of the clan SC with some distinguishing features specific for each family. Family S9 has the consensus sequence GX β XXGG (SEQ ID NO:40). Besides this consensus sequence, there is a general similarity of primary structures which classifies peptidases to this family. For instance, peptidases of this family generally have two domains, an amino-terminal domain that contains a membrane binding domain, and a carboxy-terminal domain, also referred to as the catalytic domain. The catalytic domain contains the residues of the catalytic triad. Some members of the S9 family have only the catalytic domain.

The S9 family is diverged and divided in three subfamilies: S9A, cytosolic oligopeptidases from archae and eukaryotes; S9B, eukaryotic acylaminoacylpeptidases; and S9C, dipeptidyl peptidase IV from bacteria and eukaryotes. The catalytic domain of peptidases from family S9 typically begin at about residue 400 of SEQ ID NO:30 and include the remaining carboxy-terminal amino acids (see, e.g., Fulop, et al., (1998) *Cell* 94, 161-170). Despite structural similarities to peptidases from the S9 family, the tripeptidyl-peptidase activity of PTP-A is unusual for this family of enzymes, and no other known similar activity has so far been attributed to any other member of the S9 family. In fact, all strict tripeptidyl-peptidases belong only to the subtilisin family (S8) and S33 family of serine peptidases; however, they neither share a structural relationship with PTP-A nor have activity limited to cleavage after proline residues. In particular, there are no other known prolyl tripeptidyl peptidases with an activity that is increased by iodoacetamide relative to the same prolyl tripeptidyl peptidase in the absence of iodoacetamide under the same conditions. Iodoacetamide is a compound that is traditionally a peptidase inhibitor. Typically, the activity of a prolyl tripeptidyl peptidase is increased about two-fold. Furthermore, unlike oligopeptidases, the prolyl tripeptidyl-peptidases of the present invention can cleave target peptides having as few as 4 amino acids but also target peptides having at least 30 amino

acids or a molecular weight of at least 3,000 Da. In these respects, the *P. gingivalis* tripeptidyl peptidase is a unique enzyme, and the isolation and characterization of this novel bacterial prolyl peptidase will facilitate the development of therapies to inhibit the activity of the bacterial peptidases.

5 Examples of putative prolyl-dipeptidyl peptidases are DPP-H1 (SEQ ID NO:43), DPP-H2 (SEQ ID NO:44), and DPP-H3 (SEQ ID NO:45). These peptidases have a significant percentage amino acid similarity with DPP IV and PTP-A (see Fig. 6). Each dipeptidyl peptidase is expected to have enzymatic activity, as each has a well preserved catalytic triad (Fig. 4). DPP IV has been
10 characterized and the gene encoding the peptidase has been cloned, however the substrate specificity has not been well characterized. DPP IV has been found to cleave SEQ ID NOs:6, 20, 23, and 24. DPP IV has been purified in two forms. One of the forms is a full length gene translation product containing a blocked amino-terminal residue. The second form had the amino-terminal amino acid
15 sequence HSYRAAVYDYDVRRLVKPLSEHVG (SEQ ID NO:48), which corresponds to residues 116-140 of DPP IV (Kiyama, M., et al. (1998) 1396, 39-46), indicating that it was proteolytically truncated on the amino-terminus.

 In *P. gingivalis*, PTP-A and DPP IV activity is cell surface associated. While not intending to be limiting, it is conceivable that the enzyme is membrane
20 anchored through a putative signal sequence which is not cleaved but remains as a membrane spanning domain similar to other members of the prolyl oligopeptidase family. However, a significant portion of the purified PTP-A has a truncated N-terminus, apparently due to cleavage by Lys-specific peptidase and likely to be an artifact which has occurred during the purification procedure. Nevertheless,
25 membrane bound PTP-A and DPP IV is proteolytically cleaved and shed during cultivation of the bacteria, as indicated by variable amount of soluble activities found in cell free culture media. The cell surface localization of PTP-A supports a putative physiological function in providing nutrients for growing bacterial cells. The inability of asaccharolytic *P. gingivalis* to utilize free amino acids makes the
30 bacterium entirely dependant on an external peptide supply. In this regard, PTP-A and DPP IV activities are probably very important, if not indispensable, for bacterial growth, and inhibition of prolyl tripeptidyl-peptidases and dipeptidyl-peptidases may inhibit the *in vivo* growth of organisms, including *P. gingivalis*.

For instance, treatment of *P. gingivalis* cultures in lagphase (i.e., the period after inoculation of a culture and before the organism begins to divide) and early logarithmic growth with the inhibitors PEFABLOCK and 3,4-dichloroisocoumarin inhibits growth of *P. gingivalis*.

5 Preferably, a polypeptide of the invention, preferably a prolyl peptidase, contains the amino acid sequence GXSEXG (SEQ ID NO:39), most preferably, GXSEXGG (SEQ ID NO:40), where G is glycine, X is any amino acid, and S is the active site serine. The active site serine can be identified by, for instance, labeling with diisopropylfluorophosphate as described herein. Preferably, the catalytic
10 domain of the prolyl tripeptidyl-peptidases of the invention begins at about residue 400 of SEQ ID NO:30 and includes the remaining carboxy-terminal amino acids and the corresponding amino acids of SEQ ID NOs:43-45 (see Fig. 6), more preferably, at about residue 502 of SEQ ID NO:30 and includes the remaining carboxy-terminal amino acids and the corresponding amino acids of SEQ ID
15 NOs:43-45 (see Fig. 6), most preferably, at about residue 556 of SEQ ID NO:30 and includes the remaining carboxy-terminal amino acids and the corresponding amino acids of SEQ ID NOs:43-45 (see Fig. 6).

 The invention further includes a polypeptide, preferably a prolyl tripeptidyl-peptidase, that shares a significant level of primary structure with SEQ ID NO:30.
20 The two amino acid sequences (i.e., the amino acid sequence of the polypeptide and the sequence SEQ ID NO:30) are aligned such that the residues that make up the catalytic triad, i.e., the serine, aspartic acid, and the histidine, are in register, then further aligned to maximize the number of amino acids that they have in common along the lengths of their sequences; gaps in either or both sequences are permitted
25 in making the alignment in order to place the residues of the catalytic triad in register and to maximize the number of shared amino acids, although the amino acids in each sequence must nonetheless remain in their proper order. The percentage amino acid identity is the higher of the following two numbers: (a) the number of amino acids that the two sequences have in common within the
30 alignment, divided by the number of amino acids in SEQ ID NO:30, multiplied by 100; or (b) the number of amino acids that the two sequences have in common within the alignment, divided by the number of amino acids in the candidate polypeptide, multiplied by 100. Preferably, a prolyl tripeptidyl peptidase has

greater than 35 % identity, more preferably at least about 40 % identity, most preferably at least about 45 % identity with SEQ ID NO:30. Preferably, amino acids 154-732 of SEQ ID NO:30 are used, more preferably amino acids 400-732 of SEQ ID NO:30 are used. An isolated polypeptide comprising an amino acid
5 sequence having a percentage amino acid identity of greater than 35 % with SEQ ID NO:30.

In general, the amidolytic activity of the polypeptides of the invention, preferably prolyl peptidases, can be measured by assay of the cleavage of a target polypeptide in the presence of prolyl peptidase and a buffer. Preferably, the lower
10 ratio of prolyl tripeptidyl-peptidase to target polypeptide is at least about 1:1, more preferably at least about 1:100, even more preferably at least about 1:1,000, most preferably at least about 1:10,000. Preferably, the higher ratio of prolyl peptidase to target polypeptide is no greater than about 1:10,000,000, more preferably no greater than about 1:1,000,000 and most preferably no greater than about
15 1:100,000. Buffers in which a prolyl peptidase is active are suitable for the assay. Preferably, the buffer is about 200 mM HEPES (N-2-hydroxyethylpiperazine,N'-2-ethansulfonic acid), more preferably about 50 mM HEPES, most preferably about 20 mM HEPES. Preferably, the pH of the buffer is at least about pH 6.0 and no greater than pH 8.0, more preferably about pH 7.5. Preferably, the temperature of
20 the assay is at about 37°C. The assay can be carried out for at least about 1 minute to no greater than 24 hours. Preferably, the amidolytic activity of the prolyl peptidases are measured at a prolyl peptidase:target polypeptide ratio of at least about 1:100 to no greater than 1:1,000,000 in about 200 mM HEPES, about pH 7.5 at about 37°C for at least about 3 hours. In general, the time of the assay can vary
25 depending on the substrate and enzyme:substrate ratio. Typically, target peptides are stable under these conditions, and typically it is difficult to detect background levels of hydrolysis in the absence of a prolyl peptidase. Preferably, the assay is allowed to continue until at least 1 % of the target peptide is hydrolyzed.

Prolyl-tripeptidyl peptidases of the present invention preferably are
30 inhibited by a compound chosen from the group consisting of PEFABLOCK (4-(2-aminoethyl)-benzenesulfonyl-fluoride hydrochloride), diisopropylfluorophosphate, and 3,4-dichloroisocoumarin, more preferably PEFABLOCK and diisopropylfluorophosphate, and most preferably diisopropylfluorophosphate. The

peptidases of the present invention are preferably not inhibited by a compound chosen from the group consisting of leupeptin, antipain, E-64, pepstatin, α_1 -proteinase inhibitor, α_1 -antichymotrypsin and α_2 -macroglobulin, most preferably. Significantly and unexpectedly, the amidolytic activity of a prolyl-tripeptidyl
5 peptidase of the present invention is increased by iodoacetamide relative to the prolyl-tripeptidyl peptidase in the absence of iodoacetamide under the same conditions. Preferably, the effect of iodoacetamide on amidolytic activity is measured by incubating in 200 mM HEPES, pH 7.6, at least about 0.1 nM of the prolyl tripeptidyl-peptidase with the inhibitor for about 15 minutes, adding about 1
10 mM of H-Ala-Phe-Pro-pHA, and incubating for at least about 1 minute before assaying for amidolytic activity. Typically, at least about 1 mM to no greater than 100 mM of inhibitor is used.

The polypeptides of the invention include a polypeptide having SEQ ID NO:30, or an active analog, active fragment, or active modification of SEQ ID
15 NO:30. An active analog, active fragment, or active modification of a polypeptide having SEQ ID NO:30 is one that has amidolytic activity by hydrolysis of the Pro-Yaa peptide bond present in a target polypeptide of the general formula $\text{NH}_2\text{-Xaa-Xaa-Pro-Yaa-(Xaa)}_n$ (SEQ ID NO:25). Active analogs of a polypeptide having SEQ ID NO:30 include prolyl-tripeptidyl peptidases having amino acid
20 substitutions that do not eliminate hydrolysis of SEQ ID NO:25 at the Pro-Yaa peptide bond. Substitutes for an amino acid may be selected from other members of the class to which the amino acid belongs. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and tyrosine. Polar neutral amino acids include glycine, serine,
25 threonine, cysteine, tyrosine, asparagine and glutamine. The positively charged (basic) amino acids include arginine, lysine and histidine. The negatively charged (acidic) amino acids include aspartic acid and glutamic acid. Examples of preferred conservative substitutions include Lys for Arg and *vice versa* to maintain a positive charge; Glu for Asp and *vice versa* to maintain a negative charge; Ser for
30 Thr so that a free -OH is maintained; and Gln for Asn to maintain a free NH_2 .

Active fragments of a prolyl-tripeptidyl peptidase of the invention include prolyl-tripeptidyl peptidases containing deletions or additions of one or more contiguous or noncontiguous amino acids such that the resulting polypeptide will

hydrolyze SEQ ID NO:25 at the Pro-Yaa peptide bond. An example of a fragment of a prolyl-tripeptidyl peptidase is a catalytic domain. Modified prolyl-tripeptidyl peptidases include prolyl-tripeptidyl peptidases that are chemically and enzymatically derivatized at one or more constituent amino acid, including side chain modifications, backbone modifications, and N- and C- terminal modifications including acetylation, hydroxylation, methylation, amidation, and the attachment of carbohydrate or lipid moieties, cofactors, and the like. Modified prolyl-tripeptidyl peptidases will hydrolyze SEQ ID NO:25 at the Pro-Yaa peptide bond.

Prolyl peptidases can be obtained by several methods. Isolation of a prolyl-tripeptidyl peptidase present on the surface of a cell producing the peptidase typically requires lysis of the cell followed by purification methods that are well known in the art. Alternatively, cells can be treated with a detergent, for instance Triton X-100, to remove the peptidase from the cell surface. The following are nonlimiting examples of suitable protein purification procedures: fractionation on immunoaffinity, ion-exchange, hydroxyapatite, Phenyl-Sepharose HP, MonoQ HR 5/5, or MonoP columns; ethanol precipitation; reverse phase HPLC; chromatography on silica or on an ion-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75. Preferably, isolation of a prolyl-tripeptidyl peptidase from *P. gingivalis* is accomplished using a combination of hydroxyapatite, Phenyl-Sepharose HP, MonoQ HR 5/5 and MonoP column chromatography steps as described herein.

Prolyl peptidases can also be isolated from organisms other than *P. gingivalis*. Other organisms can express a prolyl-tripeptidyl peptidase that is encoded by a coding region having similarity to the PTP-A coding region. A "coding region" is a linear form of nucleotides that encodes a polypeptide, usually via mRNA, when placed under the control of appropriate regulatory sequences. The boundaries of a coding region are generally determined by a translation start codon at its 5' end and a translation stop codon at its 3' end. "Regulatory region" refers to a nucleic acid fragment that regulates expression of a coding region to which a regulatory region is operably linked. Non limiting examples of regulatory regions include promoters, transcription initiation sites, translation start sites, translation

stop sites, and terminators. "Operably linked" refers to a juxtaposition wherein the components so described are in a relationship permitting them to function in their intended manner. A regulatory element is "operably linked" to a coding region when it is joined in such a way that expression of the coding region is achieved under conditions compatible with the regulatory region. Alternatively, other organisms can express a prolyl-tripeptidyl peptidase from a recombinant coding region encoding the peptidase. The identification of similar coding regions in other organisms can be accomplished as described herein. A prolyl-tripeptidyl peptidase can be isolated using purification methods that are well known in the art.

Alternatively, the peptidase can be chemically synthesized using methods that are well known in the art including, for instance, solid phase synthesis. Examples of, for instance, coding and regulatory regions are described herein.

The expression of a prolyl-tripeptidyl peptidase by an organism other than *P. gingivalis* can be detected using specific substrates of the general formula $\text{NH}_2\text{-Xaa-Xaa-Pro-LG}$ or $\text{NH}_2\text{-Xaa-Xaa-Pro-Yaa}$ (SEQ ID NO:41), where LG is a leaving group. The leaving group can be a chromogenic or fluorogenic group known to the art. The expression of a prolyl-tripeptidyl peptidase by an organism and subsequent cleavage of a specific substrate results in a free amino acid or a free leaving group, each of which can be assayed using techniques known to those of skill in the art. Other methods can be based on immunogenic properties of PTP-A, for instance immunoassays and histochemistry, the detection of mRNA, and PCR related methods, all of which are known to one of skill in the art.

As described in the Examples, the amino acid sequence of the amino-terminal end of a PTP-A fragment was used to identify the nucleotide sequence of the PTP coding region. The nucleotide sequence was present in a publically available database containing the nucleotide sequence of the partially finished *P. gingivalis* W83 genome. However, even though the nucleotides that encode the *P. gingivalis* PTP-A were known, there was no indication that the nucleotides were in fact transcribed and translated. The data obtained from the database only contained the nucleotide sequence of a genomic clone; there was no disclosure that the nucleotides did or did not contain an open reading frame. Moreover, there is little data known to the art regarding regulatory regions required for either the transcription or the translation of a nucleotide sequence in *P. gingivalis*.

Thus, a person of ordinary skill, having the nucleotide sequence of the genomic clone, would not be able to predict that the open reading frame encoding PTP-A was transcribed or translated. Moreover, even if there was a suggestion that the open reading frame was both transcribed and translated, there is no suggestion
5 that the polypeptide encoded by the open reading frame would have the novel activity of PTP-A.

Accordingly, the present invention is directed to a nucleic acid fragment encoding a polypeptide, particularly a prolyl-tripeptidyl peptidase, active analog, active fragment, or active modification thereof. The nucleic acid fragment can
10 have a nucleotide sequence as shown in SEQ ID NO:38. Alternatively, nucleic acid fragments of the invention include those whose complement hybridize to SEQ ID NO:38 under standard hybridization conditions as described herein. During hybridization the entire nucleotide sequence of the complement can hybridize with SEQ ID NO:38. Preferably, at least about 20 nucleotides of the complement
15 hybridize with SEQ ID NO:38, more preferably at least about 50 nucleotides, most preferably at least about 100 nucleotides.

Alternatively, the nucleic acid fragment can have a nucleotide sequence encoding a polypeptide having the amino acid sequence shown in SEQ ID NO:30. An example of the class of nucleotide sequences encoding such a polypeptide is
20 SEQ ID NO:38. This class of nucleotide sequences is large but finite, and the nucleotide sequence of each member of the class can be readily determined by one skilled in the art by reference to the standard genetic code.

The identification of similar coding regions in other organisms can be accomplished by screening individual wild-type microorganisms for the presence
25 of nucleotide sequences that are similar to the coding region of PTP-A, which is shown in SEQ ID NO:38. Screening methods include, for instance, hybridization of a detectably labeled probe with a nucleic acid fragment.

Standard hybridizing conditions are a modification of the conditions used by Church et al. ((1984) *Proc. Natl. Acad. Sci. USA* 81, 1991): 0.5 M phosphate
30 buffer, pH 7.2, 7 % SDS, 10 mM EDTA, at 68°C, and three washes, each for 20 minutes in 2x SSC, 0.1 % SDS, at 65°C. Preferably, a probe will hybridize to the nucleotide sequence set forth in SEQ ID NO:38 under standard hybridizing conditions. Generally the probe does not have to be complementary to all the

nucleotides of the nucleic acid fragment as long as there is hybridization under the above-stated conditions.

“Complement” and “complementary” refer to the ability of two single stranded nucleic acid fragments to base pair with each other, where an adenine on one nucleic acid fragment will base pair to a thymine on a second nucleic acid fragment and a cytosine on one nucleic acid fragment will base pair to a guanine on a second nucleic acid fragment. Two nucleic acid fragments are complementary to each other when a nucleotide sequence in one nucleic acid fragment can base pair with a nucleotide sequence in a second nucleic acid fragment. For instance, 5'-ATGC and 5'-GCAT are complementary. The term complement and complementary also encompasses two nucleic acid fragments where one nucleic acid fragment contains at least one nucleotide that will not base pair to at least one nucleotide present on a second nucleic acid fragment. For instance the third nucleotide of each of the two nucleic acid fragments 5'-ATTGC and 5'-GCTAT will not base pair, but these two nucleic acid fragments are complementary as defined herein. Typically two nucleic acid fragments are complementary if they hybridize under the standard conditions referred to herein.

Preferred probes are nucleic acid fragments complementary to a coding region or another nucleotide sequence that encodes a prolyl-tripeptidyl peptidase. For instance, a probe can comprise a consecutive series of nucleotides complementary to a portion of SEQ ID NO:38. Preferably a probe is at least about 18 bases, more preferably at least about 21 bases, and most preferably at least about 24 bases in length. Particularly preferred probes are

TTCGATCCGGCAAAGAAATATCCTGTTATTGTCTATGTTTACGGAGGAC
CT (SEQ ID NO:36,
GTGGATGCCGATAGAATAGGAGTACATGGCTGGAGCTATGGTGGCTTT
(SEQ ID NO:37, and SEQ ID NO:38. Methods of detectably labeling a probe are well known to the art.

The nucleic acid fragment that is identified by the probe is further analyzed to determine if it encodes a polypeptide with amidolytic activity of the Pro-Yaa

peptide bond on a target polypeptide of the general formula $\text{NH}_2\text{-Xaa-Xaa-Pro-Yaa-(Xaa)}_n$ (SEQ ID NO:25). Another method for screening individual microorganisms for the presence of nucleotide sequences that are similar to the coding regions of the present invention is the polymerase chain reaction (PCR).

5 Individual wild-type microorganisms containing nucleic acid fragments encoding a prolyl-tripeptidyl peptidase can also be identified using antibody. Preferably the antibody is directed to PTP-A. The production of antibodies to a particular polypeptide is known to a person of skill in the art, and is further detailed herein.

10 The use of hybridization of a probe to a coding region present in individual wild-type microorganisms can be used as a method to identify a coding region identical or similar to a coding region present in SEQ ID NO:38. The coding region can then be isolated and ligated into a vector as described below. Two nucleic acid sequences are "similar" if the two nucleic acid sequences can be aligned so that the number of identical amino acids along the lengths of their sequences are optimized. 15 Preferably, two nucleotide acid sequences have, in increasing order of preference, preferably at least about 90 %, at least about 92 %, at least about 94%, at least about 96%, most preferably at least about 98% identity.

As mentioned above, a nucleic acid fragment of the invention can be 20 inserted in a vector. Construction of vectors containing a nucleic acid fragment of the invention employs standard ligation techniques known in the art. See, e.g., Sambrook et al, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press (1989) or Ausubel, R.M., ed. *Current Protocols in Molecular Biology* (1994). A vector can provide for further cloning (amplification of the 25 nucleic acid fragment), i.e., a cloning vector, or for expression of the polypeptide encoded by the coding region, i.e., an expression vector. The term vector includes, but is not limited to, plasmid vectors, viral vectors, cosmid vectors, or artificial chromosome vectors. Typically, a vector is capable of replication in a bacterial host, for instance *E. coli*. Preferably the vector is a plasmid.

30 Selection of a vector depends upon a variety of desired characteristics in the resulting construct, such as a selection marker, vector replication rate, and the like. Suitable plasmids for expression in *E. coli*, for example, include pUC(X), pKK223-3, pKK223-2, pTrc99A, and pET-(X) wherein (X) denotes a vector family in which

numerous constructs are available. pUC(X) vectors can be obtained from Pharmacia Biotech (Piscataway, NH) or Sigma Chemical Co. (St. Louis, MO). pKK223-3, pKK233-2 and pTrc99A can be obtained from Pharmacia Biotech. pET-(X) vectors can be obtained from Promega (Madison, WI) Stratagene (La Jolla, CA) and Novagen (Madison, WI). To facilitate replication inside a host cell, the vector preferably includes an origin of replication (known as an "ori") or replicon. For example, ColE1 and P15A replicons are commonly used in plasmids that are to be propagated in *E. coli*.

5 An expression vector optionally includes regulatory regions operably linked to the coding region. The invention is not limited by the use of any particular promoter, and a wide variety are known. Promoters act as regulatory signals that bind RNA polymerase in a cell to initiate transcription of a downstream (3' direction) coding region. The promoter used in the invention can be a constitutive or an inducible promoter. It can be, but need not be, heterologous with respect to the host cell. Preferred promoters for bacterial transformation include *lac*, *lacUV5*, *tac*, *trc*, T7, SP6 and *ara*.

10 An expression vector can optionally include a Shine Dalgarno site (e.g., a ribosome binding site), and a start site (e.g., the codon ATG) to initiate translation of the transcribed message to produce the enzyme. It can also include a termination sequence to end translation. A termination sequence is typically a codon for which there exists no corresponding aminoacyl-tRNA, thus ending polypeptide synthesis. The nucleic acid fragment used to transform the host cell can optionally further include a transcription termination sequence. The *rrnB* terminators, which is a stretch of DNA that contains two terminators, T1 and T2, is an often used terminator that is incorporated into bacterial expression systems (J. Brosius et al., (1981) *J. Mol. Biol.* 148 107-127).

20 The nucleic acid fragment used to transform the host cell optionally includes one or more marker sequences, which typically encode a polypeptide that inactivates or otherwise detects or is detected by a compound in the growth medium. For example, the inclusion of a marker sequence can render the transformed cell resistant to an antibiotic, or it can confer compound-specific metabolism on the transformed cell. Examples of a marker sequence are sequences that confer resistance to kanamycin, ampicillin, chloramphenicol, and tetracycline.

Antibodies can be produced to a polypeptide having the sequence of SEQ ID NOs:30, 43, 44 or 45, or a polypeptide having a percentage amino acid identity as described herein. Alternatively, antibodies can be made to an antigenic analog, antigenic fragment, or antigenic modification of a polypeptide having the sequence of SEQ ID NOs:30, 43, 44 or 45. An antigenic analog, antigenic fragment, or antigenic modification of a polypeptide having SEQ ID NOs:30, 43, 44 or 45 is one that generates an immune response in an animal. Antigenic analogs of a polypeptide having SEQ ID NOs:30, 43, 44 or 45 include prolyl peptidases having amino acid substitutions that do not eliminate peptide antigenicity in an animal. Substitutes for an amino acid may be selected from other members of the class to which the amino acid belongs, as described herein. Fragments of a prolyl peptidase of the invention include prolyl peptidases containing deletions or additions of one or more contiguous or noncontiguous amino acids such that the resulting polypeptide will generate an immune response in an animal. An example of a fragments of a prolyl peptidase is a catalytic domain. Modified prolyl peptidases include prolyl peptidases that are chemically and enzymatically derivatized at one or more constituent amino acids, including side chain modifications, backbone modifications, and N- and C- terminal modifications including acetylation, hydroxylation, methylation, amidation, and the attachment of carbohydrate or lipid moieties, cofactors, and the like.

Accordingly, an aspect of the invention is an immunogenic composition comprising an isolated prolyl peptidase, or an antigenic analog, antigenic fragment, or antigenic modification thereof, preferably a prolyl tripeptidyl-peptidase. The prolyl tripeptidyl-peptidase preferably has amidolytic activity for cleavage of the Pro-Yaa peptide bond present in a target polypeptide with the general formula $\text{NH}_2\text{-Xaa-Xaa-Pro-Yaa-(Xaa)}_n$ (SEQ ID NO:25), wherein the amidolytic activity is measured at a prolyl tripeptidyl-peptidase:target polypeptide ratio of at least about 1:100 to no greater than about 1:1,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours.

The immunogenic composition can further include excipients or diluents that are pharmaceutically acceptable as carriers and compatible with the immunogenic composition. The term "pharmaceutically acceptable carrier" refers to a carrier(s) that is "acceptable" in the sense of being compatible with the other

ingredients of a composition and not deleterious to the recipient thereof. Suitable excipients are, for example, water, saline, dextrose, glycerol, ethanol, or the like, and combinations thereof. In addition, if desired, the immunogenic composition may contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents, and/or adjuvants which enhance the effectiveness of the immune-stimulating composition.

The immunogenic composition can be used in a method for protecting an animal from a disease caused by *P. gingivalis*. This method includes administering the immunogenic composition and eliciting antibodies to a prolyl peptidase, antigenic analog, antigenic fragment, or antigenic modification. The diseases that can be treated in this manner include periodontal diseases, which includes gingivitis and periodontitis. Clinical hallmarks of periodontitis include loss of tooth attachment and periodontal pocket formation.

Alternatively and preferably, periodontal diseases can be treated by the use of inhibitors of a prolyl peptidase. An inhibitor of a prolyl peptidase, preferably a prolyl tripeptidyl-peptidase, can be present in a composition that preferably contains a pharmaceutically acceptable carrier. For instance, inhibitors can be applied systemically, subgingivally (e.g., subgingival irrigation) and/or by controlled release delivery directly into the periodontal pocket using methods well known to the art (see, e.g., Kornman, K., (1993) *J. Periodontol.* 64, 782-791). Preferably, an inhibitor is applied subgingivally or by controlled release delivery.

The prolyl peptidases, active analogs, fragments, and modifications thereof can be used in a method of reducing growth of bacteria *in vitro* or *in vivo*. Preferably, the bacteria is a periodontal pathogen, i.e., a bacterial pathogen that causes periodontal disease, more preferably the bacteria is *P. gingivalis*. The inability of asaccharolytic *P. gingivalis* to utilize free amino acids makes the bacterium entirely dependant on an external peptide supply. The action of the polypeptides of the invention may be required for bacterial growth, and inhibition of the polypeptides of the invention may inhibit the *in vivo* growth of organisms, including *P. gingivalis*. The method includes decreasing the amount of dipeptides and/or tripeptides (e.g., the result of cleavage of SEQ ID NO:25 by a prolyl-tripeptidyl peptidase) and the amount of free amino acids that result from further cleavage of the dipeptides and/or tripeptides present by inhibiting a prolyl

peptidase, active analog, active fragment, or active modification thereof, such that the amount of dipeptides and/or tripeptides generated by the polypeptides is decreased. The amount of dipeptides and/or tripeptides is decreased relative to the amount of dipeptides and/or tripeptides present in the absence of the inhibitor.

5 Preferably, the amount of dipeptides and/or tripeptides generated is decreased by an inhibitor, a monoclonal antibody that inhibits the prolyl peptidase, or polyclonal antibodies that inhibit the prolyl peptidase, more preferably, the amount of dipeptides and/or tripeptides generated is decreased by an inhibitor. Preferably, an inhibitor acts to inhibit a polypeptide of the invention, preferably a prolyl peptidase,
10 by blocking the active site of the polypeptide. The polypeptide can be present on the surface of the bacteria or secreted into the environment, preferably the polypeptide is present in the surface of the bacteria.

The present invention is also directed to a method of developing an inhibitor of a prolyl peptidase, active analog, active fragment, or active
15 modification thereof, preferably a prolyl-tripeptidyl peptidase. The method includes identifying a molecule that inhibits the amidolytic activity of the prolyl peptidase. This can be accomplished by, for instance, incubating the prolyl peptidase with a candidate molecule under conditions that promote amidolytic activity of the prolyl peptidase and determining if the amidolytic activity of the
20 prolyl peptidase is decreased relative to the amidolytic activity in the absence of the molecule. The amidolytic activity can be measured by cleavage of the Pro-Yaa peptide bond present in the target polypeptide SEQ ID NO:25 as described herein. One method of developing an inhibitor includes using the target peptide SEQ ID NO:25 and replacing the Xaa residues with modified amino acids. It is expected
25 that some modified amino acids will cause the target peptide to act as an inhibitor.

EXAMPLES

The present invention is illustrated by the following examples. It is to be understood that the particular examples, materials, amounts, and procedures are to
30 be interpreted broadly in accordance with the scope and spirit of the invention as set forth herein.

Example 1

Materials

Diisopropylfluorophosphate (DFP), leupeptin and 3,4-dichloroisocoumarin, were purchased from Calbiochem (La Jolla, CA). Antipain, iodoacetamide, substance P, bradykinin and bradykinin related peptides, were obtained from Sigma. Other peptides used in this study were synthesized at the Molecular Genetic Instrumental Facility (University of Georgia, Athens, GA) using Fmoc protocol with an advanced ChemTech MPS350 automated synthesizer. H-Ala-Phe-Pro-pNA, H-Gly-Pro-pNA, Z-Gly-Pro-pNA, Z-Ala-Pro-pNA, and H-Pro-pNA (where pNA is p- Nitroanilide; Z is benzyloxycarbonyl; and H is hydrogen and denotes an unblocked amino-terminal group) were obtained from Bachem (King of Prussia, PA). Prolinal was kindly provided by Dr. James Powers (Georgia Institute of Technology, Atlanta) and cystatin C by Dr. Magnus Abrahamson (University of Lund, Sweden).

Methods

Source and Cultivation of Bacteria— *P. gingivalis* HG66 was obtained from Dr. Roland Arnold (University of North Carolina, Chapel Hill), while the strains W50 (ATCC 53978) and ATCC 33277 were obtained from the ATCC. All cells were grown as described previously (Chen, Z., et al., (1992) *J. Biol. Chem.* 267, 18896-18901).

Enzyme Activity Assays— Routinely, the tripeptidyl peptidase amidolytic activity was measured with H-Ala-Phe-Pro-pNA (1 mM) in 0.2 M HEPES (N-2-hydroxyethylpiperazine,N'-2-ethansulfonic acid), pH 7.5 at 37°C. The concentration of enzyme was 0.1 nM to 1 nM. The assay was performed in a total volume of 0.2 ml on microplates, and the initial turnover rate was recorded at 405 nm using a microplate reader (Spectramax Molecular Devices, Sunnyvale, CA). In inhibition studies, the enzyme was first preincubated with inhibitor for 15 min at 37°C, substrate added, and residual activity recorded after 5 minutes to 30 minutes. H-Gly-Pro-pNA, Z-Ala-Pro-pNA, Z-Gly-Pro-pNA and H-Pro-pNA (1 mM final concentration) were assayed in the same manner.

Protein Determination—Protein concentration was determined using the BCA reagent kit (Sigma, St. Louis, MO), using bovine serum albumin as a standard.

Localization of Tripeptidyl-Peptidase Activity—Cultures of *P. gingivalis* HG66, W50 and ATCC 33277, at different phases of growth, were subjected to the following fractionation procedure. The cells were removed by centrifugation (10,000 x g, 30 minutes), washed twice with 10 mM Tris, 150 mM NaCl, pH 7.4, resuspended in 50 mM Tris, pH 7.6, and disintegrated by ultrasonication in an ice bath at 1500 Hz for 5 cycles (5 minutes sonication/5 minutes brake). Unbroken cells and large debris were removed by centrifugation (10,000 x g, 30 minutes) and the opalescent supernatant subjected to ultracentrifugation (150,000 x g, 120 minutes), yielding a pellet containing bacterial membranes and a supernatant which was considered as membrane-free cell extract. All fractions, as well as the full culture, culture medium, and full culture after sonication, were assayed for amidolytic activity against H-Ala-Phe-Pro-pNA.

Enzyme Purification—All purification steps were performed at 4°C except for FPLC separations, which were carried out at room temperature. Cells were harvested by centrifugation (6,000 x g, 30 minutes), washed with 50 mM potassium phosphate buffer, pH 7.4, and resuspended in the same buffer (150 ml per 50 gram of cells wet weight). Triton X-100 (10% volume/volume in H₂O) was added slowly to the bacterial cell suspension to a final concentration of 0.05%. After 120 minutes of gentle stirring, unbroken cells were removed by centrifugation (28,000 x g, 60 minutes). Proteins in the supernatant were precipitated with cold acetone (-20°C) added to a final concentration of 60% and collected by centrifugation. The pellet was redissolved in 50 mM potassium phosphate buffer, pH 7.0, and extensively dialyzed against 20 mM potassium phosphate, pH 7.0, containing 0.02% sodium azide. The dialyzed fraction was clarified by centrifugation (28,000 x g, 30 min) and applied to a hydroxyapatite column (BioRad, Melville, NY) equilibrated with 20 mM potassium phosphate, pH 7.0, at a flow rate of 20 ml/hour. After equilibration, the column was washed until the A₂₈₀ fell to zero. Bound proteins were eluted with a gradient from 20-300 mM potassium phosphate and fractions (7 ml) analyzed for dipeptidyl- and tripeptidyl-peptidase activity using H-Gly-Pro-pNA and H-Ala-Phe-Pro-pNA, respectively. The activity against the latter

substrate was pooled, saturated with 1 M ammonium sulfate, clarified by centrifugation, and directly loaded onto a Phenyl-Sepharose HP (Pharmacia, Piscataway, NJ) column equilibrated with 50 mM potassium phosphate, pH 7.0, containing 1 M ammonium sulfate. The column was washed with two volumes of equilibration buffer, followed by buffer containing 0.5 M ammonium sulfate, and developed with a descending gradient of ammonium sulfate from 0.5 to 0 M. Active fractions were pooled, extensively dialyzed against 20 mM Tris, pH 7.5, and applied to a MonoQ HR 5/5 FPLC column equilibrated with the same buffer. The column was washed with 5 volumes of equilibration buffer at 1.0 ml/minute, following which bound proteins were eluted with a gradient of 0- 300 mM NaCl. The active fractions were pooled, dialyzed against 25 mM Bis-Tris, pH 6.3, and subjected to chromatofocusing on a MonoP FPLC column equilibrated with Bis-Tris buffer, using a pH gradient developed with 50 ml of 10x diluted Polybuffer 74 (Pharmacia), adjusted to a pH of 4.0.

Electrophoretic Techniques— The SDS-PAGE system of Schagger and von Jagow (Schagger, H., and von Jagow, G. (1987) *Anal. Biochem.* 166, 368-379), was used to monitor enzyme purification and estimate the enzyme molecular mass. For amino-terminal sequence analysis, proteins resolved in SDS-PAGE were electroblotted to polyvinylidene difluoride membranes using 10 mM CAPS, pH 11, 10% methanol (Matsudaira, P. (1987) *J. Biol. Chem.* 262, 10035-10038). The membrane was washed thoroughly with water and stained with Coomassie Blue G250. The blot was air dried, and protein bands cut out and subjected to NH₂-terminal sequence analysis with an Applied Biosystems 491 Protein Sequencer using the program designed by the manufacturers.

Enzyme Fragmentation —The purified prolyl tripeptidyl peptidase (PTP-A) was partially denatured by incubation in 6 M urea in 0.02 M Tris, pH 7.6, for 60 minutes. Low molecular mass gingipain R (RgpB) (Potempa, J., et al. (1995) *Prospect. Drug Discovery and Design* 2, 445-458) from *P. gingivalis* was then added to make an enzyme:substrate molar ratio of 1:100. The reaction mixture was made in 1 mM cysteine and the sample incubated overnight at 37°C. Generated peptides were separated by reverse-phase HPLC using a μ Bondapak C-18 column (3.9 x 300 mm) (Waters, Millford, MA). Peptides were eluted with 0.1% trifluoroacetic acid and acetonitrile containing 0.08% trifluoroacetic acid, using a

gradient from 0 to 80% acetonitrile over 60 minutes. Peptides were monitored at 220 nm and collected manually.

For determination of the active site serine residue and to confirm that the purified enzyme was a serine peptidase, 100 µg of purified PTP-A was first
5 incubated with 170 µCi of [1,3-³H]DFP (Amersham, Arlington Heights, IL) for 30 minutes at 25°C in 20 mM HEPES, pH 7.5. The reaction was quenched by addition of cold DFP to a final concentration of 10 mM and the radiolabelled material analyzed by SDS-PAGE, followed by autoradiographic analysis. The gel was dehydrated, soaked in PPO solution for 2 hours, dried, and the DFP-binding
10 proteins detected by fluorography after an exposure time of 96 hours on X-ray film (XAR; Kodak, Rochester, NY). The bulk of radiolabelled protein was subjected to proteolytic fragmentation with RgpB and peptides obtained separated by reverse-phase HPLC as described above. Radioactivity in each peptide fraction was measured using a β liquid scintillation counter, and the labeled peptide, as well as
15 other selected peptides were subjected to sequence analysis.

Identification of the PTP-A Gene— The database containing the unfinished *P. gingivalis* W83 genome, available from The Institute for Genomic Research, was searched for the presence of nucleotide sequences corresponding to the NH₂-terminal and the internal PTP-A amino acid sequences using the TBLASTN
20 algorithm, BLAST version 2.0.8, and the default values for all parameters (Altschul, S.F., et al., (1997) *Nucleic Acid Res.* 25, 3389-3402). An identified clone gnl | TIGR | *P. gingivalis*_126 was retrieved from The Institute for Genomic Research data base (<http://www.tigr.org>). The position of the PTP-A gene was localized using the NCBI open reading frame (ORF) finder (available from the
25 National Center for Biotechnology Information, at <http://www.ncbi.nlm.nih.gov/gorf/gorf.html>). The amino acid sequence, obtained by conceptual translation of the entire ORF, was further used for homology screening by use of the NCBI BLAST search tool.

Enzyme Specificity— Peptides were incubated with 1 µg PTP-A at an
30 enzyme:substrate molar ratio of 1:100 for 3 hours or 24 hours in 50 µl of 200 mM HEPES, pH 7.5, at 37°C, and the reaction stopped by acidification with trifluoroacetic acid. The samples were then subjected to reverse-phase high

pressure liquid chromatography using a μ Bondapak C-18 column (3.9 x 300 mm) (Waters, Millford, MA) and an acetonitrile gradient (0-80 % in 0.075% trifluoroacetic acid in 50 min). Each peak, detected at 220 nm, was collected, lyophilized, re-dissolved in 50% (volume/volume) methanol, 0.1% acetic acid and subjected to analysis by mass spectrometry.

Mass Spectrometry—A Finnigan MAT 95S, sector mass spectrometer (Finnigan MAT, Bremen, Germany) equipped with an electrospray source (ESI) was used operated essentially as described previously (Stenfors, C., et al., (1997) *J. Biol. Chem.* 272, 5747-5751). Peptides were identified by fitting of the obtained spectra to specific sequences using an Internet application program MsFit available at <http://falcon.ludwig.ucl.ac.uk/msfit.html>.

Example 2

Enzyme Localization, Purification and Initial Characterization

Analysis of amidolytic activity against H-Ala-Phe-Pro-pNA in several fractions of *P. gingivalis* HG66, W50 and ATCC 33277 clearly indicated that an enzyme(s) with prolyl tripeptidyl-peptidase activity is localized on the cell surface in all strains tested with less than 5% of the total activity being found in the medium regardless of the growth phase of the bacterial culture. Cell associated enzyme was easily detached from the bacterial surface by treatment with a low concentration (0.05%) of Triton X-100. This procedure released more than 85-90% of activity in a soluble form. Subsequent acetone precipitation of proteins in the Triton X-100 fraction successfully separated the activity from pigment which remained in solution. The redissolved protein fraction, after dialysis, was applied to hydroxyapatite (100 ml) equilibrated with 20 mM potassium phosphate buffer pH 7.0. The elution was carried out with 20 mM potassium phosphate buffer pH 7.0, using a phosphate gradient from 20 mM to 300 mM at flow rate 20 ml/h. At this step substantial separation of the PTP-A activity from both the DPP IV and bulk protein was achieved (Fig. 1a). Further purification performed by subsequent chromatography steps including Phenyl-Sepharose (Fig. 1b), MonoQ (Fig. 1c) and MonoP columns (Fig. 1d), resulted in the isolation of purified enzyme.

Phenyl-Sepharose HP (25 ml) was equilibrated with 50 mM potassium phosphate, 1M ammonium sulfate, pH 7.0, at flow rate 30 ml/h. The column was

washed with two volumes of equilibration buffer and a step gradient of 0.5 M ammonium sulfate was applied, following which a descending gradient of 0.5 to 0 M ammonium sulfate was applied. The PTP-A containing fractions were extensively dialyzed against 20 mM Tris-HCl, pH 7.0, and concentrated by ultrafiltration. The concentrated PTP-A containing fractions were applied to a MonoQ column equilibrated with the same buffer. The column was washed with 5 volumes of equilibration buffer, following which bound protein was eluted with a gradient of 0-300 mM NaCl. The concentrated fraction of PTP-A from the MonoQ column was equilibrated with 25 mM Bis-Tris, pH 6.3, and loaded on a MonoP column equilibrated with the same buffer. A pH gradient was developed using 50 ml of Polybuffer 74, with the pH adjusted to 4.0.

Significantly, the chromatography step on the MonoP column yielded the A_{280} profile much sharper than the activity peak. Although this imperfect overlap of protein and activity may suggest that the protein component does not represent the active enzyme, the rest of data argues with such a contention. This apparent contradiction may be likely explained by the enzyme inhibition by the reaction product of H-Ala-Phe-Pro-pNA hydrolysis but this possibility has not been explored. The yield of protein and activity recovery in a typical purification procedure is summarized in Table 1.

Table 1. Purification of the PTP- A from *P. gingivalis*

Step	Volume (ml)	Protein (mg)	Total activity*	Specific activity (units/mg)	Purification fold	Yield (%)
Triton X-100 extract after centrifugation	200	1200	757 673	642	1	100
Acetone precipitate	50	600	537 622	896	1.4	71
Hydroxyapatite chromatography	50	22	400 039	18 183	28	53
Phenyl-Sepharose	48	10	312 505	31 250	48	41
MonoQ	3	1.5	244 828	163 218	254	32
MonoP	4	0.7	188 400	269 142	420	25

* Based on the enzymatic activity using H-Ala-Phe-Pro-pNA where one unit = mOD/min/1ml

SDS-PAGE analysis of the purified enzyme revealed the presence of two protein bands with apparent molecular masses of 81.8 and 75.8 kDa, respectively (Fig. 2, lane f). Autoradiography of the enzyme sample radiolabeled with [1,3-³H]DFP (Fig. 2, lane g) clearly indicated that the bands represented either two distinct serine peptidases or different molecular mass forms of the same enzyme. In an attempt to distinguish between these two options, the electrophoretically resolved proteins were subjected to amino terminal sequence analysis. Unfortunately, it was found that the 81.8 kDa form of PTP-A had a blocked N-terminus. In contrast, the sequence NH₂-SAQTTRFSAADLNALMP (SEQ ID NO:23) was found at the N-terminus of the lower molecular mass form of the enzyme. This result led us to the possibility that the 75.8 kDa form of PTP-A was derived from the 81.8 kDa form through proteolytic cleavage of a 6 kDa amino-terminal peptide. To confirm this hypothesis and, in addition, to localize the active site residue within *P. gingivalis* PTP-A, the mixture containing both radiolabeled enzymes was proteolytically fragmented and peptides resolved by reverse-phase HPLC. This procedure yielded only one major radioactive peptide peak, and the purified peptide was found to have a single amino acid sequence: IGVHGWXYGGFMTTNL (SEQ ID NO:24), where X apparently represents the active-site serine residue covalently and irreversibly modified by DFP. These data convincingly indicate that the two protein bands of purified PTP-A represents different forms of the same enzyme. The portion of the purified PTP-A having a truncated N-terminus may be due to cleavage by Lys-specific peptidase and is likely to be an artifact which occurred during the purification procedure. Nevertheless, the proteolytic shedding of membrane bound PTP-A also occurs during cultivation of the bacteria, as indicated by variable amount of soluble activities found in cell free culture media.

Example 3

pH Optimum, Stability and Inhibition Profile

Using the amidolytic activity assay with H-Ala-Phe-Pro-pNA it was found that the enzyme has a broad pH optimum from pH 6.0 to 8.0 and in 0.2 M HEPES, pH 7.6 was stable for at least 12 hours at 25°C or 37°C. PTP-A activity was not affected by class specific synthetic inhibitors of cysteine or metalloproteinases

(Table 2). In contrast, preincubation of the enzyme with DFP or PEFABLOCK resulted in total loss of activity, supporting its classification as a serine peptidase. Surprisingly, however, 3,4-dichloroisocoumarin was only a poor inhibitor, and PMSF, leupeptin, antipain and prolinal had no effect at all. Interestingly, preincubation of PTP-A with iodoacetamide, but not with N-ethylmaleimide, stimulated enzyme amidolytic activity about two-fold. Human plasma inhibitors, such as α_1 -proteinase inhibitor, α_1 -antichymotrypsin and α_2 -macroglobulin did not affect the enzyme activity, nor were they cleaved by PTP-A.

The effect of inhibitors on amidolytic activity of DPP IV was also determined using the same conditions as those used for PTP-A, but using H-Gly-Pro-pNA as a substrate.

Table 2. Effect of inhibitors on the amidolytic activity of PTP-A and DPP IV.
Results are for a 15-min incubation at 37 C in 0.2 HEPES pH 7.6,
with 1 mM H-Ala-Phe-Pro-pNA as substrate.

	Inhibitor	Concentration	Residual activity of PTP-A, %	Residual activity of DPP IV, %
5	Diisopropyl fluorophosphate	10 mM	0	0
		10 mM	96	20
10	Phenylmethanesulfonyl fluoride	1mg/ml	20	15
		10mg/ml	0	0
	PEFABLOC SC	1 mM	56	100
15	3,4-dichloroisocoumarin	5mM	200	100
	Iodoacetamide	5 mM	100	100
	N-Ethylmaleimide	1 mM	98	100
20	1,10- orthophenanthroline	5 mM	93	100
		0.1 mM	100	100
	EDTA	0.1 mM	100	100
25	Leupeptin	0.1 mM	100	20
	Antipain	10 mM	100	0
30	Proinal	10 mM	100	30
	Val-Pro	10 mM	100	1
35	Ala-Pro			
	Ala-Gly-Pro			

Example 4

Substrate Specificity

Among several chromogenic substrates tested, including H-Ala-Phe-Pro-pNA, H-Gly-Pro-pNA, Z-Gly-Pro-pNA, Z-Ala-Pro-pNA, H-Pro-pNA, only H-Ala-Phe-Pro-pNA was hydrolyzed by PTP-A indicating a prolyl specific tripeptidyl-peptidase activity. To further confirm this specificity several synthetic peptides composed of 5 to 34 amino acid residues and containing at least one proline residue were tested as substrates for PTP-A. Out of 22 peptides tested only those with a proline residue in the third position from the amino terminal end were cleaved (Table 3), with the significant exception of peptides with adjacent proline residues (peptides 3, 4 and 16). In addition, a free α -amino group was absolutely required for cleavage after the third proline residue as exemplified by resistance to enzymatic hydrolysis of peptide 9, which differs from the peptide 8 only in acylation of the α -amino group of the N-terminal valine residue. Except for these two limitations, the peptide bond -Pro-↓-Yaa- was cleaved at the same rate in all peptides with the general formula $\text{NH}_2\text{-Xaa-Xaa-Pro-Yaa-(Xaa)}_n$ (SEQ ID NO:25), where Xaa represents any amino acid residue while Yaa could be any residue except proline, regardless of the chemical nature of the amino acids and the length of the peptide. In all cases the reaction was completed within 3 hours and prolonged incubation for 24 hours did not affect the pattern of cleavage, confirming the absolute requirement for a proline residue at the third position from the unblocked N-terminus. In addition, these data indicate that the preparation of PTP-A was free of any contamination with either aminopeptidase, dipeptidyl peptidase, or endopeptidase activities.

The cleavage specificity of DPP IV was also determined using the same conditions as those used for PTP-A. The results (Table 3) demonstrate that DPP IV does not cleave between two proline residues.

Table 3. Cleavage specificity of PTP-A and DPP IV on synthetic peptides.

Substrate	Cleavage site	SEQ ID NO:
Peptide 1	H-Arg-Pro- Pro -l-Gly-Phe-Ser-Pro-Phe-Arg	1
Peptide 2	H-Arg-Pro- Pro -l-Gly-Phe	2
Peptide 3	H-Lys-Arg-Pro- Pro -Gly-Phe-Ser-Pro-Phe-Arg	3
Peptide 4	H-Tyr-Arg-Pro- Pro -Gly-Phe-Ser-Pro-Phe-Arg	4
Peptide 5	H-Arg-Pro-Hyp-Gly-Phe-Ser-Pro-Phe-Arg	5
Peptide 6	H-Arg-Pro-l-Lys-Pro-l-Gln-Gln-Phe-Phe-Gly-Leu-Met-NH ₂	6
Peptide 7	H-Val-Pro- Pro -l-Gly-Glu-Asp-Ser-Lys-Glu-Val-Ala-Ala-Pro-His-Arg-Gln	7
Peptide 8	H-Val-Pro- Pro -l-Gly-Glu-Asp-Ser-Lys	8
Peptide 9	Ac-Val-Pro- Pro -Gly-Glu-Asp-Ser-Lys	9
Peptide 10	H-Val-Glu-Pro-l-Ile-Pro-Tyr	10
Peptide 11	H-Arg-Gly-Pro-l-Phe-Pro-Ile	11
Peptide 12	H-Ala-Arg-Pro-l-Ala-D-Lys-amide	12
Peptide 13	H-Pro-Asn-Pro-l-Asn-Gln-Gly-Asn-Phe-Ile	13
Peptide 14	H-Arg-His-Pro-l-Lys-Tyr-Lys-Thr-Glu-Leu	14
Peptide 15	H-Gly-Val-Pro-l-Lys-Thr-His-Leu-Glu-Leu	15
Peptide 16	H-Lys-Gly-Pro- Pro -Ala-Ala-Leu-Thr-Leu	16
Peptide 17	H-Gln-Lys-Gln-Met-Ser-Asp-Arg-Glu-Asn-Asp-Met-Ser-Pro-Ser-Asn-Val-Val-Pro-Ile-His-Val-Pro- Pro -Thr-Thr-Glu-Asn-Lys-Pro-Lys-Val-Gln	17
Peptide 18	H-Phe-Leu-Arg-Glu-Pro-Val-Ile-Phe-Leu	18
Peptide 19	H-Gly-Ile-Arg-Pro-Tyr-Glu-Ile-Leu-Ala	19
Peptide 20	H-Leu-Pro-l-Asp-Leu-Asp-Ser-Ser-Leu-Ala-Ser-Ile-Gln-Glu-Leu-Ser-Pro-Gln-Glu-Pro-Arg-Pro- Pro -Glu-Ala	20
Peptide 21	H-Cys-Leu-Ser-Ser-Gly-Thr-Leu-Pro-Gly-Pro-Gly-Asn-Asp-Ala-Ser-Arg-Glu-Leu-Glu-Ser	21
Peptide 22	H-Lys-Ile-Ala-Gly-Tyr-His-Leu-Glu-Leu	22
Peptide 23	H-Ser-Pro-l-Tyr-Ser-Ser-Asp-Thr-Thr	46
Peptide 24	H-Ala-Pro-l-Val-Arg-Ser-Leu-Asn-Cys-Thr-Leu-Arg-Asp-Ser-Gln-Gln-Lys	47
! indicates cleavage site mediated by PTP-A		
! indicates cleavage site mediated by DPP IV		

The lack of cleavage after internal proline residues in the synthetic peptides corresponds well with the absence of any proteolytic activity on several protein substrates including IgA, IgG, albumin, azocasein, carboxymethylated ribonuclease and gelatin. However, the size of substrate, which is a limiting factor in the activity of oligopeptidases (Walter, R., et al., (1980) *Mol. Cell. Biochem.* 30, 111-126), is not restricting in the case of PTP-A, because the enzyme is able to cleave a tripeptide (NH₂-Xaa-Xaa-Pro) from the N-terminus of both human cystatin C and interleukin 6.

Example 5

PTP-A Sequence Analysis

Partial PTP-A amino acid sequence data allowed us to identify the *P. gingivalis* genomic clone gnl | TIGR | *P. gingivalis*_126 in the Unfinished Microbial Genomes data base, TIGR. An ORF corresponding to the PTP-A amino acid sequence was found as indicated by the fact that all sequences of the PTP-A derived peptides obtained by the enzyme polypeptide fragmentation with RgpB were present in the protein primary structure inferred from the nucleotide sequence of the ORF. The 732 amino acid polypeptide with a calculated mass of 82, 266 Da was encoded in this ORF. The homology search performed using the NCBI TBLASTN tool against GenBank+EMBL+DDBJ+PDB databases and subsequent multiple sequence alignments using the ClustalW Multiple Sequence Alignment tool (Fig. 3) indicated that PTP-A is a new member of the prolyl oligopeptidase (S9) family of serine peptidases (Rawlings, N.D., et al., (1991) *Biochem. J.* 279, 907-908).

The sequence GX SXGG (SEQ ID NO:40) is a signature feature for the S9 family of serine peptidases. Within this large and diverse S9 family of evolutionary and functionally related enzymes both from prokaryotes and eukaryotes, PTP-A was most closely related to bacterial dipeptidyl peptidase IV (DPP IV) from *Flavobacterium meningosepticum*, *Xantomonas maltophilus*, and *P. gingivalis*, sharing 31.6%, 30.4%, and 28.5% amino acid sequence identity, respectively. Remarkably, the COOH-terminal region of the PTP-A molecule (residues 502 - 732) shows a significant similarity to the eukaryotic prolyl oligopeptidases with 34% and 33% identity to human DPP IV and mouse fibroblast activation protein (FAP), respectively (Fig. 3). This part of the molecule contains the amino acid

residues which encompass the catalytic triad in all characterized prolyl oligopeptidases, and from the multiple alignments with DPP IV of confirmed active site residues (Kabashima, T., et al., (1995) *Arch. Biochem. Biophys.* 320, 123-128) it is apparent that Ser-603, Asp-678 and His-710 represent the catalytic triad of PTP-A (Fig. 3). Such an inference is further supported by the direct labeling of Ser-603 by DFP. In addition, the computer assisted search for sequential motifs characteristic for transmembrane domains revealed the presence of such a putative region within the N-terminal sequences of PTP-A, with residues 5 to 25 most likely folded into a hydrophobic α -helix responsible for membrane anchoring of this enzyme.

In *P. gingivalis* PTP-A, as well as in DPP IV, all activities are cell surface associated, and it is conceivable that the enzymes are membrane anchored through putative signal sequences which are not cleaved but remain as a membrane spanning domain similar to other members of the prolyl oligopeptidase family. The cell surface localization of di- and tripeptidyl-peptidases suggests a putative physiological function in providing nutrients for growing bacterial cells. Here, the inability of asaccharolytic *P. gingivalis* to utilize free amino acids (Dashper, S.G., et al., *J. Dent Res.* 77, 1133 (Abstract) (1988)) makes the bacterium entirely dependant on an external peptide supply. In this regard, DPP-IV and PTP-A activities are probably very important, if not indispensable, for bacterial growth.

This suggestion is strongly corroborated by the fact that the *P. gingivalis* genome contains three additional genes encoding peptidases homologous with DPP-IV and PTP-A and one related to aminopeptidase B. The peptidases homologous with DPP-IV and PTP-A are referred to as homologs H1 (SEQ ID NO:43), H2 (SEQ ID NO:44), and H3 (SEQ ID NO:45) (Fig. 6). If expressed, each gene product would probably have enzymatic activity because each has a well preserved catalytic triad (Fig. 4). In addition, all of these genes encode a putative signal peptide which may act in providing membrane-anchorage motifs.

Example 6**Influence of Proteinase Inhibitor on *P. gingivalis* Growth**

To evaluate whether *P. gingivalis* growth was influenced by the presence of a peptidase inhibitor, *P. gingivalis* in logphase growth was diluted 1:5 into liquid media and incubated at 37°C. The cell density was monitored by measuring the optical density at 600 nm (OD₆₀₀). When the optical density began to increase, Pefabloc was added at 0.5 mg/ml or at 2.0 mg/ml. The control culture received no Pefabloc. The cultures receiving Pefabloc exhibited decreased growth (Figure 5). The peptidase inhibitor had to be added before the culture reached an OD₆₀₀ of about 0.3 for the peptidase inhibitor to have an effect on growth.

The complete disclosures of all patents, patent applications, publications, and nucleic acid and protein database entries, including for example GenBank accession numbers and EMBL accession numbers, that are cited herein are hereby incorporated by reference as if individually incorporated. Various modifications and alterations of this invention will become apparent to those skilled in the art without departing from the scope and spirit of this invention, and it should be understood that this invention is not to be unduly limited to the illustrative embodiments set forth herein.

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Sequence Listing Free Text

- SEQ ID NOs:1-11: Synthetic peptides
- SEQ ID NO:12: Target peptide
- SEQ ID NOs:13-22: Synthetic peptides
- 25 SEQ ID NO:23: Amino-terminus of the lower molecular mass form of PTP-A.
- SEQ ID NO:24: Amino acid sequence present in PTP-A, where X apparently represents the active-site serine residue covalently and irreversibly modified by DFP.
- 30 SEQ ID NO:25: Target peptide, where Xaa represents a natural or modified amino acid residue, Yaa represents a natural or modified amino acid residue except proline, and N is equal to or greater than 1.
- SEQ ID NO:26: Mouse fibroblast activation protein

- SEQ ID NO:27: Human DPP IV
- SEQ ID NO:28: DPP from *Flavobacterium meningosepticum*
- SEQ ID NO:29: DPP from *P. gingivalis*
- SEQ ID NO:30: *P. gingivalis* PTP-A
- 5 SEQ ID NO:31: Portion of PTP-A
- SEQ ID NO:32: Portion of DPP from *P. gingivalis*
- SEQ ID NO:33: Portion of H1 homolog of *P. gingivalis* DPP
- SEQ ID NO:34: Portion of H2 homolog of *P. gingivalis* DPP
- SEQ ID NO:35: Portion of H3 homolog of *P. gingivalis* DPP
- 10 SEQ ID NOs:36-37: Probes
- SEQ ID NO:38: Nucleotide sequence of coding region encoding PTP-A.
- SEQ ID NO:39: Consensus sequence for clan SC where X is any amino acid and S is the active site serine GXSTXXG.
- SEQ ID NO:40: Consensus sequence for family S9 where X is any amino acid and S is the active site serine GXSTXGG.
- 15 SEQ ID NO:41: A specific substrate for a prolyl-tripeptidyl peptidase, where Xaa represents a natural or modified amino acid residue, and Yaa represents a natural or modified amino acid residue except proline.
- 20 SEQ ID NO:42: DPP from *P. gingivalis*
- SEQ ID NO:43: H1 homolog of *P. gingivalis* DPP
- SEQ ID NO:44: H2 homolog of *P. gingivalis* DPP
- SEQ ID NO:45: H3 homolog of *P. gingivalis* DPP
- SEQ ID NO:46: Synthetic peptides
- 25 SEQ ID NO:47: Synthetic peptides
- SEQ ID NO:48: Amino terminal sequence of DPP IV

What is claimed is:

1. An isolated prolyl tripeptidyl-peptidase, active analog, active fragment, or active modification thereof having amidolytic activity for cleavage of a peptide bond present in a target polypeptide having at least 4 amino acids, wherein the prolyl tripeptidyl-peptidase:target polypeptide ratio is at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours.
2. An isolated prolyl tripeptidyl-peptidase, active analog, active fragment, or active modification thereof having amidolytic activity at a prolyl tripeptidyl-peptidase:target polypeptide ratio of at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours, and wherein the prolyl tripeptidyl-peptidase is isolated from *P. gingivalis*.
3. The isolated prolyl tripeptidyl-peptidase of claim 2 wherein the peptide cleaved by the isolated prolyl tripeptidyl-peptidase comprises the sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:11, H-Ala-Arg-Pro-Ala-D-Lys-amide, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:25, and SEQ ID NO:37.
4. The isolated prolyl tripeptidyl-peptidase of claim 2 wherein the amino acid sequence of the isolated prolyl tripeptidyl-peptidase comprises the amino acid sequence GXSEXG (SEQ ID NO:39).
5. The isolated prolyl tripeptidyl-peptidase of claim 4 wherein the amino acid sequence of the isolated prolyl tripeptidyl-peptidase comprises the amino acid sequence GXSEXG (SEQ ID NO:40).
6. The isolated prolyl tripeptidyl-peptidase of claim 4 wherein the amino acid sequence of the isolated prolyl tripeptidyl-peptidase comprises SEQ ID NO:30.

7. An isolated polypeptide, active analog, active fragment, or active modification thereof having amidolytic activity for cleavage of a peptide bond present in a target polypeptide having at least 4 amino acids, wherein the polypeptide:target polypeptide ratio of at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours.
8. An isolated polypeptide comprising an amino acid sequence having a percentage amino acid identity of greater than 35 % with SEQ ID NO:30.
9. An isolated nucleic acid fragment encoding a prolyl-tripeptidyl peptidase, active analog, active fragment, or active modification thereof, having amidolytic activity for cleavage of a peptide bond present in a target polypeptide having at least 4 amino acids, wherein the prolyl tripeptidyl-peptidase:target polypeptide ratio of at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours.
10. The nucleic acid fragment of claim 9 wherein the nucleic acid fragment has a nucleotide sequence comprising SEQ ID NO:38.
11. The nucleic acid fragment of claim 9 wherein a complement of the nucleic acid fragment hybridizes to SEQ ID NO:38 under hybridization conditions of 0.5 M phosphate buffer, pH 7.2, 7 % SDS, 10 mM EDTA, at 68°C, followed by three for 20 minutes washes in 2x SSC, and 0.1 % SDS, at 65°C, wherein at least about 20 nucleotides of the complement hybridize.
12. An isolated nucleic acid fragment encoding a polypeptide wherein the polypeptide comprises an amino acid sequence having a percentage amino acid identity of greater than 35 % with SEQ ID NO:30.
13. A method of identifying an inhibitor of a prolyl-tripeptidyl peptidase, active analog, active fragment, or active modification thereof, comprising identifying a molecule that inhibits the amidolytic activity of the prolyl-

tripeptidyl peptidase by incubating the prolyl-tripeptidyl peptidase with the molecule under conditions that promote amidolytic activity of the prolyl-tripeptidyl peptidase and determining if the amidolytic activity of the prolyl-tripeptidyl peptidase is inhibited relative to the amidolytic activity in the absence of molecule.

14. A method of reducing growth of a bacterium comprising inhibiting a prolyl tripeptidyl-peptidase, active analog, active fragment, or active modification thereof, by contacting the prolyl tripeptidyl-peptidase with an inhibitor of the prolyl tripeptidyl-peptidase.
15. A method for protecting an animal from a periodontal disease caused by *P. gingivalis* comprising administering to the animal the inhibitor of claim 14 wherein the disease is selected from the group consisting of gingivitis and periodontitis.
16. The method of claim 15 wherein the inhibitor is administered by a method selected from the group consisting of subgingival application and controlled release delivery.
17. A method of reducing growth of a bacterium comprising inhibiting a prolyl dipeptidyl-peptidase, active analog, active fragment, or active modification thereof, by contacting the prolyl dipeptidyl-peptidase with an inhibitor of the prolyl dipeptidyl-peptidase.
18. An immunogenic composition comprising an isolated prolyl tripeptidyl-peptidase, or an antigenic analog, antigenic fragment, or antigenic modification thereof, the prolyl tripeptidyl-peptidase having amidolytic activity for cleavage of a peptide bond present in a target peptide having at least 4 amino acids, wherein the prolyl tripeptidyl-peptidase:target polypeptide ratio is at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours.
19. The immunogenic composition of claim 18 further comprising an adjuvant.

20. A composition comprising an inhibitor of an isolated prolyl tripeptidyl-peptidase and a pharmaceutically acceptable carrier.
21. A dipeptidyl peptidase having an amino acid sequence comprising SEQ ID NO:43.
22. A dipeptidyl peptidase having an amino acid sequence comprising SEQ ID NO:44.
23. A dipeptidyl peptidase having an amino acid sequence comprising SEQ ID NO:45.

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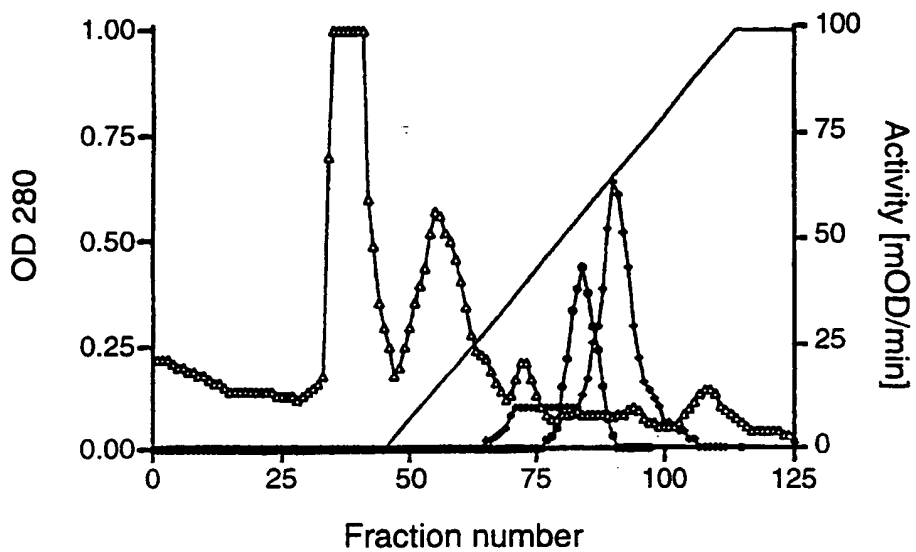


Fig. 1a

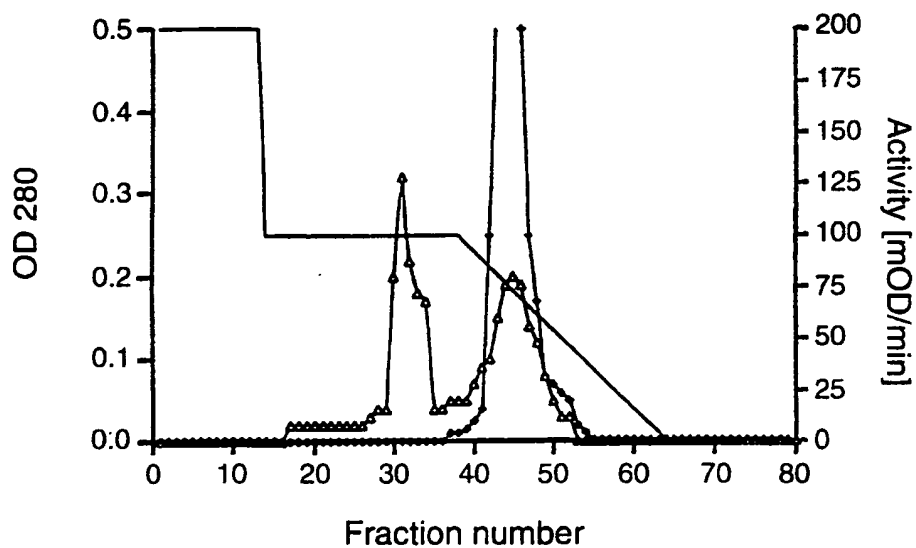


Fig. 1b

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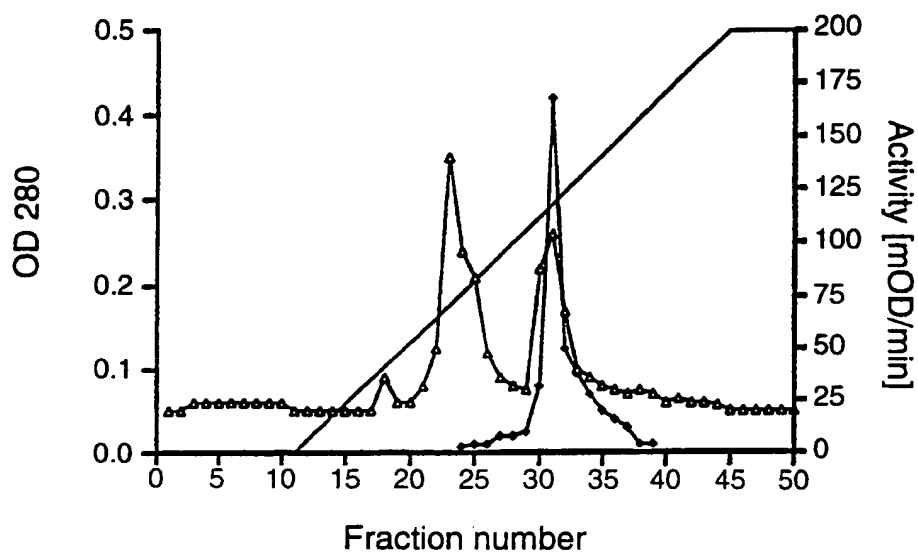


Fig. 1c

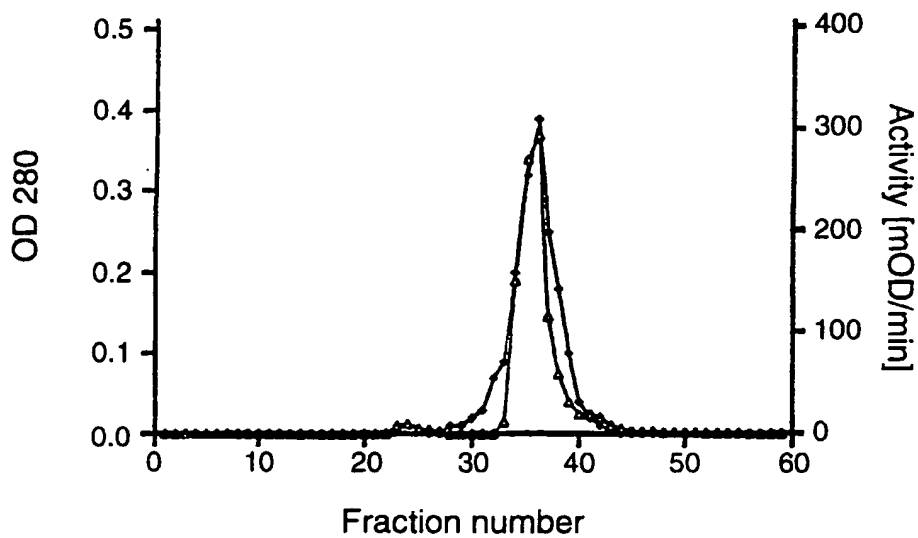


Fig. 1d

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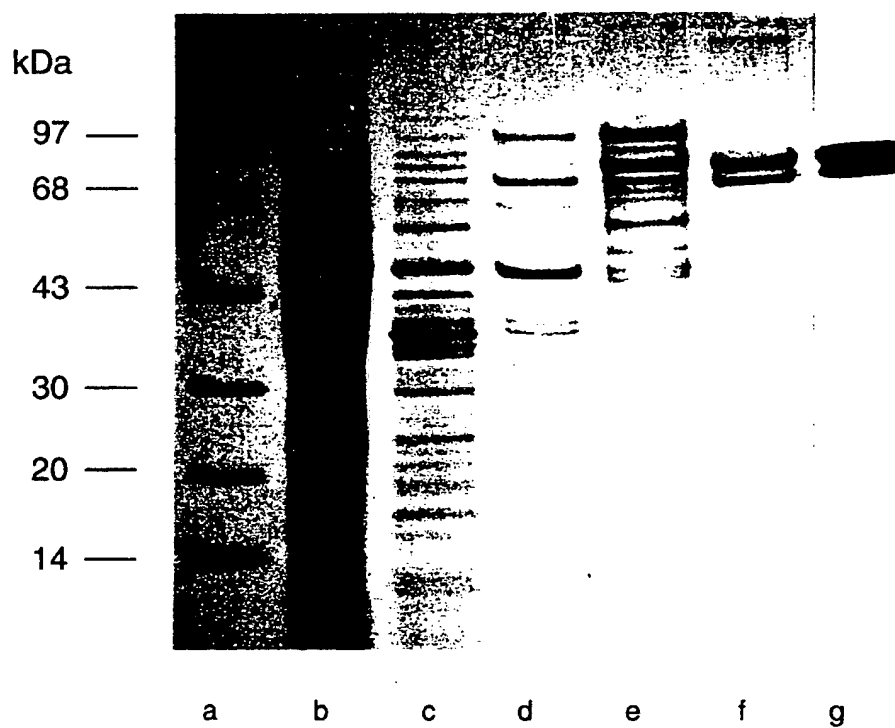


Fig. 2

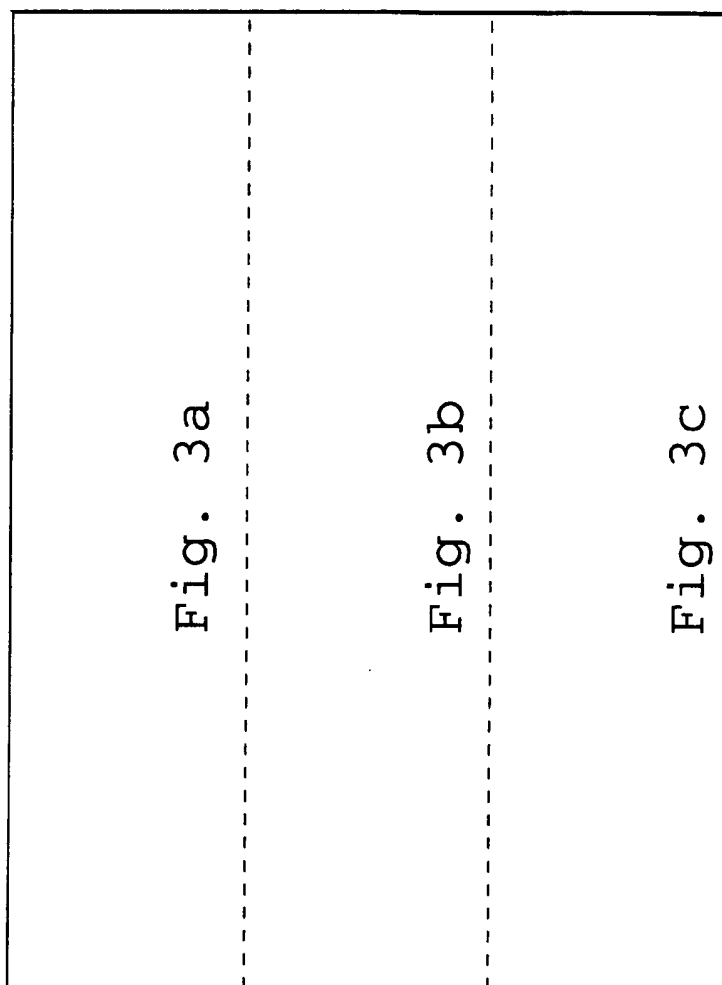


Fig. 3

SEQ ID NO:	
26 Mm-FAP	1 MKTWLAVTVEGTTAAALAVVLCIVLRPSR-VYKPEGNTK-RALT LKDI L NGTFSYKTYF
27 Hs-DPP	1 MKTPWRVLLGLGAAALVTITVTPVVLLNKGTDADTSR-KTYTLDYLNKNTYRLKLYS
28 Fm-DPP	1 ---MKKKILFSLLSIAVAVAFHGLSAQEITLDKITYSGQYRAK-GISGIIASLND---
29 Pg-DPP	1 -MKRPVTHLLIGIVTMCMAAQTKGNKFPVDLKEITSGMFYARSAGSGIRSMPD---
30 PTP-A	1 ---MKRIIFQQLFLSVCAITVALPCSAQSPETSGKEFTLEQLMPGCKEFYN-FYPEYVV
Mm-FAP	59 PNWISSEQEYLHQSEDDNIVFVNIETRE--SYIIISNSTMKS VN--ATDYGISPDQRQFY
Hs-DPP	60 LRWISDHEYLYK--QENNILVFNAEYEN--SVFLFENSTFDEFHGSINDYSLSPDGQFTL
Fm-DPP	48 ----GENYATH--EPTGIANKSYKITSQ--KEKNIVDGSFQGYT----FSNDESK--ITL
Pg-DPP	51 ----GEHYTEMNRERTALIRKNYASGKAVDITLFSVERARECPFKQIQNIYEVSSSTGHHTL
	56 GLQWMCNDNYVFIE---GDDLIVENKANEKSAQITRFSAADLNALMPEGCKFOTIDAFPSFR
Mm-FAP	114 LESDYSKLRMSYTAIVYIYVDLQNGEFVRYGVELPRPIQYTLQSPVCGSKIAVYVONNIYTLK
Hs-DPP	116 LEYNYVKQWRHSYTAISYDIYDLNKRQLITEERI PNNTQWITLSPVGHKLA VYVNNILYVK
Fm-DPP	92 LQKSSQSIYRHSFLGKEFEVKDLKSEITVSLNNANWIOE-PKFSPDGSKVAFIADNNLFYQ
Pg-DPP	106 LFTDMESIYRHSYRAAVYDYVRRNLVKPLSEHVGVKVMIPTESPDGRMVAFVRDNNITFK
	113 TLDAGRCGLVVLFTQGGVLVGFIDMLARKVTYLFDTNEETASLDFSPVGD RVAYVRNHNLYIA
Mm-FAP	174 QRP--GPPFQITVYTGRENRIIFNGITPDWVYEEEMLATKYALWSPDCKFLAMVEFNDSDI
Hs-DPP	176 IEP--NLPSYRLTWTKEDITIVNGIHDWVYEEEFVSAYSALWSPNETELAMAOQFNDTEV
Fm-DPP	151 DLN--TGKITITTDGKKNFILNGLCDWVYEEEFEGHADYYQNN-KACDALVFVREDEKVV
Pg-DPP	166 KFD--FQTEVQVITDGOINSILNGATDWYEEEFQVTNLMSSMS-ADNAFLAVRSDESAY
	173 RGGKLGEGMSRAIAVTIDGTETLVYGOAVHQREFGIEKGTFWIS-PKESCLAFYRMDQSMV
Mm-FAP	232 PLIAYSYYGCG--QYFRTINIPYKAGAKNPVVRVFTVDTTYPHVG---PMEMPVVPEMI
Hs-DPP	234 PLIEYSFYSDESLQVPKTVRVPYKAGAVNPTVKFFVNTDLSSTVNTATSIQITAPASM
Fm-DPP	208 PEHNPPIYYQN--LYPKLMTYKVPKAGEENSATVAVLYQLSSKSAQ---LNFGSSEKY
Pg-DPP	223 PEYRMPMYEK--LYFEDYTKVPKAGEKNTVSLIHLVNVADRNTKS---VSLPIDADG
	232 KPTPLVDYHP--LEAESKPLVYEMAGTPSHHVTVGIVYHLA QCKIVY---LQTGEKEK

Fig. 3a

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Mm-FAP	287	ASSDYVFSWLTWVSSERVCTQWLKRVQNVSMISICDFREDHWAWECPKNQEHVEESRTGM
Hs-DPP	294	LFGDHYLCDVTWATQERISLQWLRIQNYSMDCDYDESSGRWNCCLVARQHEEMSTTGM
Fm-DPP	262	YIIPQLFQTN---ANDEIVATARRHQNKVDLLKNTKTAASV-----K-LFTEITDPAW
Pg-DPP	277	YIIPRTAFID---NADEIAVMTINRLQNDQFKMYVHPKSLVPK-----LILQDMNKRY
	285	ELTNLSWSP---DENILYVAEVNRAQNECKVNAYDAETGRFVR-----TLFVEITDKHY
Mm-FAP	347	AGGFFVSTPAFESQDATSYKIFSDKDGVKHITHVLKDTVENAIOITSGKMEATYIFRMTQD
Hs-DPP	354	VGRFRPSEPHFILLDENSFYKIIISNEGGYRHICYEQIDKDCFTFKGTWEVIGIPEAITSD
Fm-DPP	311	LETDMLT-MEELDDNS--FLWASERDGHRLVWYDAAGKLLKQVSKGCDWEHINYYGYNPK
Pg-DPP	326	MDSDWLTQTLKEFITGEG--FAYVSEKDGFAHYLYLDNRKGVHRRITSGNMIVTKLYGVNAS
	335	MEPLHP--LTFLPGSNNOQFIWQSRDRDGMNHLXYLTGRLIRQVITKGEWEVTNFAGFDPK
Mm-FAP	407	SLFYSSNEFEGYPGRRNIRYRISIGNSPPSKKCVTCILRKERCQYVTASIFS YKAKY YALVC
Hs-DPP	414	YLYYISNEYKGMPPGRNLKYLQLSDYTKVT-CLSCENPERCQYYSVSFSKEAKY YQLRC
Fm-DPP	368	---TKEVVIQIIEKGSINKVSKLNINTG---KTQLLSNAEGNNSAFAFSKTFNVFINTS
Pg-DPP	384	-----GTVFYQSADESPRPAVYDAIDAKGR---KIKLSLVGTN-DALFSGNYAYYINTY
	393	-----GTRLVFESEIPEASPLERHFYCIDIKGG---KTKDLTPESGMHRTQLSPDGSAILDIF
Mm-FAP	467	Y-GPGIPISITLHDGRDQEIQVLEENKELENSIRNIQIPKVEIKKIK-DGGTLTFWKMITL
Hs-DPP	473	S-GPGIPLYITLHSSVNDKGLRVLIEDNSALDKMLONVQMPSSKLLDFHIL-LNETKFWYQMITL
Fm-DPP	421	S-TAKVPTKYITLKDANGKDVKEIQNDDLLNKLKSDNFIKKEFITHPNAAQDQMNAMWIK
Pg-DPP	435	SSAATPAVVSVFRSKGAKELRITLEDVALLRERELKAYRYPNKEFTTKTQSSCLELNAWIVK
	446	Q-SPTVERKVTVTNIG-KGSHITLLEAKNPDTGYAMPEIRTGTMMAAD--GQTPLYKILTM
Mm-FAP	525	PPQFDRSKKKYPLITQVYGGPCSQSKSVFAVN---WITYLASKEGIVIALVDGRGTAFQGG
Hs-DPP	531	PPHFDSKKYPLITQVYAGPCSQKADIVFRLN---WATYLASTENIIVASHDGRGSGYQGG
Fm-DPP	480	PKNEFDPKKYPVEMFQYSGPGSQQVANSWDGGNGIMFDMLAQKG-YLVVQVVDGRGTGFRG
Pg-DPP	495	PIDFDP SRHYPLVMQVSGNSQQLDRYSFD---MEHYLASKG-YVVAQVVDGRGTGARG
	502	PLHEDPAKKYPVIMVYVGGFHAQIMTKTNRSSVSGGDIYMAQKG-MAVFTVDSRGSAIRFG

Fig. 3b

Mm-FAP	582	DKELHAYMVKKLGVVEVEDQITAVRKFIEMGFIDEERIALWWSYGGYVSSIALASGIGLF
Hs-DPP	588	DKIMHAINRRRLGTFEVEDQTEAARQFSKMGFVDNKRIALWWSYGGYVTSMLGSGSGVF
Fm-DPP	539	TKYKKVTVKKNLGVVEEDQITAAKWLGNQSYVTKSRIGIFGWSYGGYMASIAMTKGADV
Pg-DPP	551	SEWRKCTVMQLGVFEESDDQITAAATATIGQLPVVDAARIGWWSYGGYITLMSLCRGNELF
	561	AAFEQVIHRRRLGQTEMAEQMCEVDFLKSQSWVDADRIQVHEWSYGGFMITINIMLTHGADV
		* →
Mm-FAP	642	KCGIAPVSSWENYASIVSERFMGLFTKDDNLEHYKNSIVMARAERYFRNVDYLLIHGTA
Hs-DPP	648	KCGIAPVSRWENYESVYTERFMGLFTPEDNLDHYRNSIVMSRAENFKQVEYELLIHGTA
Fm-DPP	599	KMGIAVAPVTVNRFYDSIVTERFLQTPQENK--DGYDLNSPTTYAKLLKG-KFLLIHGTA
Pg-DPP	611	KAGIAPVADWRFYDSVYTERFMRTPKENA--SGYKMSAIDVASQLQG-NLLIVSSSA
	621	KVGAGGPVLDNRYEITMYGERYFDAPQENP--EGYDAANLLKRGDLKG-RIMLIHGAI
		* →
Mm-FAP	702	DDNVHFQNSAQIAKALVNAQVDFQAMVYSDQNHGTSSEFSONHLYITIMTHFLKQCFSLSD
Hs-DPP	708	DDNVHFQNSAQISKALVDVGVDFQAMVYIDEDHGIIASSTAHQHIYTHMSHFIKQCFSLP-
Fm-DPP	656	DDNVHFQNSMEFSEALIQKKQDFDMPDKNVHSIIIGCNTFRPQLYERKVTNYILEN----
Pg-DPP	668	DDNVHLQNTMLFTEALVQANLPEDMAIYMDKNHSIIYGGCNTFRNHLVTRKAKFLFDNL----
	678	DFVVMQHSLSLFLDACMKARTYPDYVYVYPSHEHNMVMPD-RVHLYETIIRYFTDHL----

Fig. 3c

		SEQ ID NO:
PTP-A	556	717
DPP	499	661
DPP-H1	350	524
DPP-H2	640	810
DPP-H3	495	667
		*

Fig. 4

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Influence of Pefablock-serine proteinase inhibitor on *P. gingivalis* growth.

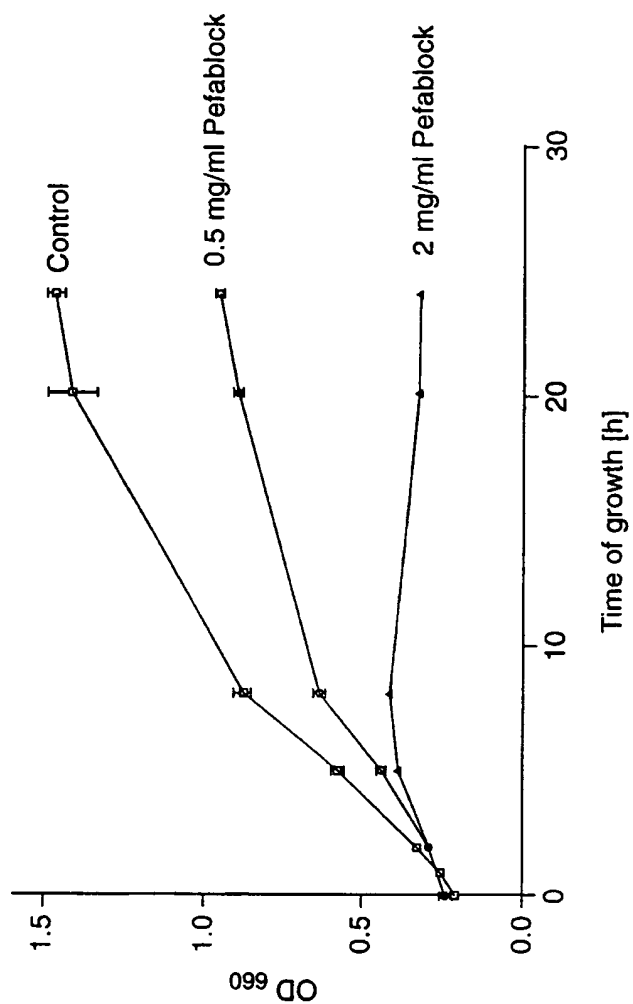


Fig. 5

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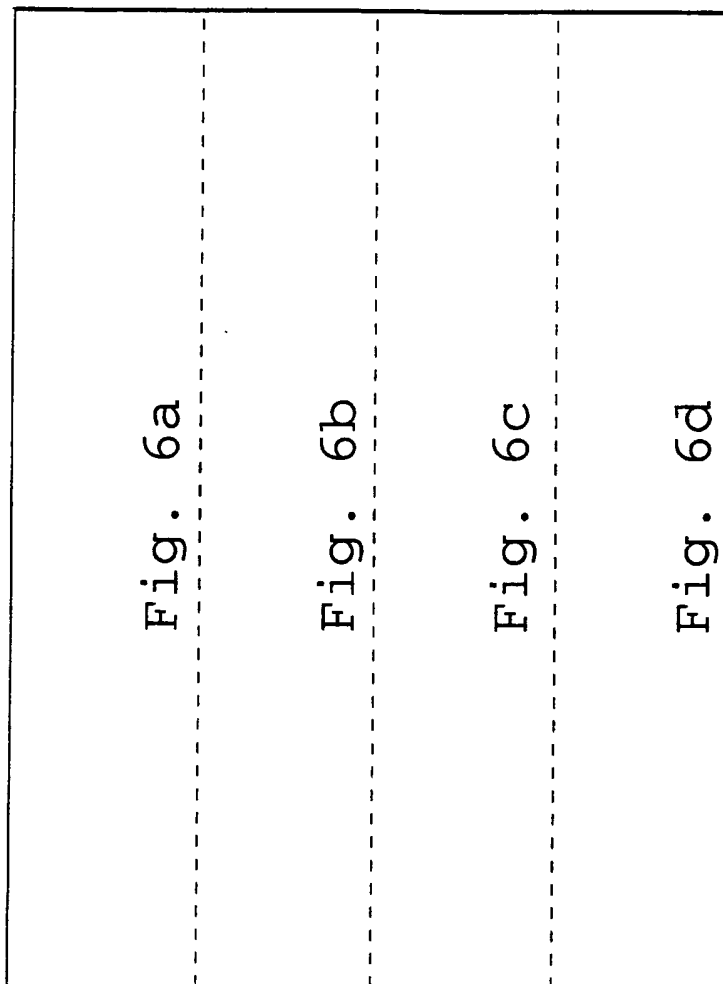


Fig. 6

[illegible]

Fig. 6a

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126PP 201 -VHQREFGTEKG--TFMSPKGSLAFVFM--DQS-MVKPTPIVDYH---PI
 87PP 144 WYEEEFVGNL--MSASADNAFLAFVS--DES-AVPEYRMPMYED--KL
 65PP 112 -LATGEFRLLK--THDDTFGVAFNYA--SKN-KDEAYVLNLD--S
 101PP 241 ARGNILLNNEKEALGMPHEDMLMVERKEGNAKRLVAFPMGKGEKTLVSNLPESQFRM
 9PP 170 ATGRIITDLMYK--HMDWEVETPHPI--AN-ATDGMITGKD--II

126PP 243 EAESKPLVYPMAGT--PSHHIVTVGYHHLA--TG-KTVYLOTGEPEKEKFLTNISMSPD
 87PP 188 YPEDYTKYPKAGE--KNSITVSLHYNVA--DR-NTKSVSPIDADGYIPRLAETDNA
 65PP 153 DK-TRIVLYDLKQN--K--ITREIFANE--DY-DVSGHLHS-RK--
 101PP 301 SPDAVYLYFYKQEKGPCKDPLFIRHLPDDDRQSDWRDRSQIYLLNAESGVYGPTEFGYST
 9PP 210 ME-GEPEAEPMKPW--S-GIEDFSWSP--DG--QNIAYASRKKTG--

126PP 296 NILVVAE--VNRAQNECKVNAQDAETGEFVRTLFEVETDKHVEP--LH-P--LHLEP
 87PP 241 DELAVMT--LNRLQNDFKM--YVHPKSLVPKLILODKNRVYVSDWIO-T--LKEFTT
 65PP 188 -R--N-YEIDLMA--VEGEKSVVVPVSATYKELKKLME--KEFK--
 101PP 361 TYVMDIAPDSKRALIGTLSTDWTRRPFRFATIMEYNMETGKADTLITRDPSIDALQYTPD
 9PP 247 -MAYSLS--TN--SDIYII--YNLASGRTHNISEGMMGYDTYPK--FSPD

126PP 346 CSNNQFIHWDSR-RDGMNHLMT--VDITGRLIHQVTKGEWEVTNFA--G
 87PP 292 CCG--FAYVSE-KDGFATHT--YDNKGVTHRRITSGNWDVTKL--G
 65PP 224 GKE--FSVM--D--YDD--
 101PP 421 GRH--LIVMGS-ADAFGNIGNLKSGVTPNSYDKQFFLDLSIRKATADIKNPNPSVSAG
 9PP 287 GKS--IAWISMERDGYES--DLKRLFVADLAFGKRTHMNPTFDYNNVDMI

Fig. 6b

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126PP 389 -[P]P[K]G[IR]L[Y]F[E]S[T]E[A]S[P]L[E]R[H]F[Y]C[I]I[K]G[K]T[K]D[L]T[P]-E[S]G[M]H[R]T[Q]L[S]P[D]-G[S]A[L]I[D]I[F]
87PP 333 -V[E]A[S]C[H]-V[F]Y[Q]S[A]E[E]S[P]I[R]R[A]V[A]L[A]K[G]R[K]T[K]-L[S]L-N[V]G[T]N[D]A[L]F[S]G[N]-Y[A]Y[Y]N[T]Y
65PP 235 --D[E]--[I]-L[L]I[A]V[Q]S[D]K[Y]G[T]Y[Q]F[D]I[R]--T[K]-----K[F]I-----L[L]Y[D]-L
101PP 478 R[E]D[R]K[N]N-Y[M]F[R]A[E]N-G-S[R]K[Q]L[Y]R[E]L[E]K[T]L[E]I[S]Q[T]G[E]D[V]V[Q]W[F]G[V]A[D]N[G]A[V]W[Y]S[G]Q
9PP 332 Q[M]A[P]D[S]K[G]I[Y]F[L]A[C]K[E]A--E[T]N[L]W[E]H[L]K[T]G[I]R[Q]I[T]Q[G]H[D]Y[A]D[F]S[V]R[N]D---V[M]L[A]K[R]

126PP 446 Q[S]P[T]V[E]R[K]V[M]V[N]I[G]K[G]S[H]T[L]L[E]A[K]N[P]D[T]G[Y]A[M]P[E]L[I]R[T]G-----T[I]M[A]A[D]G[Q]T[P]L[Y]Y[K]I[T]
87PP 388 S[S]A[A]T[E]A[V]S[V]F[R]S[K]C[A]K[E]L[R]T[L]E[D]N[V]A[L]R[E]R[L]K[A]Y[R]N[P]K[E]F[T]T[I]K[T]Q[S]G-L[E]L[N]A[M]I[V]
65PP 269 ----M[E]Q[L]K-----E[E]D-----M[A]E[M]R[P]I-----K[F]K[S]R[D]G-L[T]I[H]G[F]I[T]
101PP 536 S[A]N[N]A[D]R[L]Y[R]D[G]T[K]G[K]L[V]W[D]S[A]E[K]L[A]N[I]D[F]T[P]A[R]D[W]N-----Y[T]A[P]D[G]-T[V]V[E]G[W]Y[Y]
9PP 387 H[S]F[E]L[P]D[D]L[Y]R[V]N[L]K[N]G[A]A[Q]A[V]T[A]E[N]K[V]I[L]D[R]I[T]P[T]C[E]K[R]-----W[N]K[I]I[T]D[G]-G[N]M[L]T[W]V

126PP 501 M[E]L[H]F[D]P[A]K[K]Y[P]M[L]V[Y]V[G]G--P[H]A[Q]L[V]T[K]T[W]R[S]S[V]G[G]W[D]I[Y]M[A]Q[K]G[Y]A[V]F-T[V]D[S]R[G]S[A]N
87PP 447 K[E]I[D]E[D]S[R]H[Y]P[V]L[M]V[Q]V[S]G--P[N]S[Q]Q[V]L[D]--R[Y]S[F]D-WE[H]Y[L]A[S]K[G]V[M]V[A]C[V]D[G]R[G]T[G]A
65PP 299 L[E]K[A]A[L]E[G]K[K]V[P]L[I]V[N]P[H]G[G]-P--Q[E]I[R]D--S[W]G[E]N[P]E[T]Q[L]F[A]S[R]G[Y]A[T]L[Q]A[N]F[R]I[S]G[G]
101PP 589 L[P]Q[F]D[S]K[K]Y[P]M[L]V[Y]V[G]G[T]S[P]I[N]R[T]L[E]G--H[Y]S[L]A---M[Y]A[A]Q[G]Y[V]Y[T]N[P]S[G]I[T]G
9PP 443 L[P]N[E]D[K]N[K]Y[P]A[I]I[Y]C[Q]G[G]-P--Q[N]T[V]S-Q[F]M[S]F[R]W[N]L[R]L[M]A[E]Q[G]Y[I]V[I]A[P]R[H]G[V]P[G]

126PP 559 R[G]A[A]F[E]Q[V]I[H]R[R]L[G]Q[T]E[M]A[D]Q[M]C[G]V[D]-F[L]K[S]Q[S]W[V]D[A]D[R]I[G]V[H]G[S]Y[G]G[F]M[I]T[N]L[M]L[T]H[G]
87PP 502 R[G]E[E]M[R]K[T]Y[M]Q[L]G[V]F[E]S[D]D[Q]I[A]A[T]-A[I]G[Q]L[P]Y[V]D[A]A[R]I[G]I[W]C[S]Y[G]G[Y]I[L]M[S]I[L]C[R]G[N]
65PP 353 Y[G]K[E]F[L]R[A]G[F]K[Q]I[G]R[K]A[M]D[V]E[D]G[V]R-V[A]I[S]Q[Q]W[V]D[P]D[R]I[A]I[Y]G[A]S[H]G[E]Y[A]I[L]M[G]L[M]K[T]P
101PP 643 Y[G]Q[E]Y[A]A[R]H[V]N[A]M[G]D[R]T[A]D[E]I[L]G[A]T[K]E[F]I[R]T[H]S[F]V[N]G[K]K[V]G[C]E[F]G[A]S[Y]G[G]F[M]Q[Y]O[T]K[T]-
9PP 498 F[G]Q[K]W[N]E[Q]I[S]G[D]Y[G]G[N]M[P]R[E]Y[L]T[A]V[D]-E[M]K[K]E[P]V[D]S[D]R[I]G[A]V[G]A[S]Y[G]G[G]F[S]V[Y]W[L]A[G]H[D]

```

Fig. 6c

126PP 618 DVEKVGVAAGPMI-----D-----MN--RYEIMYGERYFDA--PQENPEGYD--AANLLK
 87PP 561 GTEKAGTAVAPVA-----D-----MR--FYDSVYTERFMRT--PKENASGYK--MSSALD
 65PP 412 DLYACGVYGVSNITYTFDGSFPEYMK--PFKEMVKEIIVYDLDNPEEAAIAKE--VSFFQ
 101PP 702 DIFAAAMSHAGISSIS--N-----YMGSGYWGCGYSTVASTDSYPMNNDIYAGHSHLFR
 9PP 557 KREAAFIHAGIFNLEMQYATTEEMFA--NWDIGGPFWEKEN--VVAQRTYA--TSHKF

126PP 662 RAGDLKGRIMLIHGADDPVVMVQHSILFLDACVKARTYPDYVYPSHEHNMGPD--RVHEL
 87PP 605 VASQLQGNLIIVSGSADDNVHLQNTMLFTALVQANIPFDMAIYMDKNHSIYGGNTRYHL
 65PP 469 ID-KINKPLFVVQGANDPRVNNINESDQIVTALRARGFEVPMVKYNECHGFHRENSMEL
 101PP 755 AD-KIHITPLILLHGSMVDINVPТАESVNLVYNAKILGREVEFIEFTQDHFILPEPERIRW
 9PP 612 MQ-NWDTPILMIHGELDFRILLASQMAAFDAQLRGVPSMLIYPPDENHNVLOEQNALLF

126PP 721 YETITRYETDHL-----
 87PP 665 YTRKAKFLFDNL-----
 65PP 528 YRAMLGFFAKHLKK-----
 101PP 814 TNSICAWFAFWLQDDPTWNNELYPPVNL
 9PP 671 HRIFFGWLDRWLKK-----

Fig. 6d

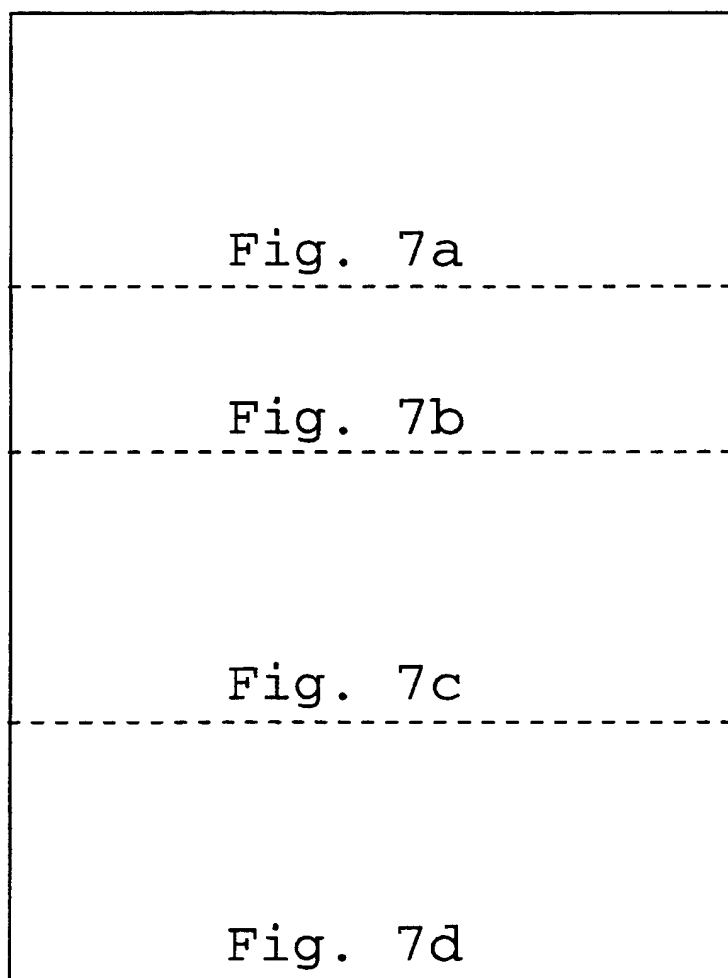


Fig. 7

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P. gingivalis W 83 PTP sequence

SEQ ID NO: 38 13228 atgaagaagacaatcttccaacaactatctgtctgtttgtgcc
 SEQ ID NO: 30 M K K T I F Q Q L F L S V C A
 13273 cttacagtggccttgcccttggtcggctcagtcctcctgaaacgagt
 L T V A L P C S A Q S P E T S
 13318 ggtaaggagtttactccttgagcaactgatgcccgaggagaaaagag
 G K E F T L E Q L M P G G K E
 13363 ttttataacttttaccgccgaatacgtgggtcggtttgcaatggatg
 F Y N F Y P E Y V V G L Q W M
 13408 ggagacaattatgtctttatcgagggtgatgatttagtttttaat
 G D N Y V F I E G D D L V F N
 13453 aaggcgaatggcaaatacggctcagacgaccagattttctgtctgcc
 K A N G K S A Q T T R F S A A
 13498 gatctcaatgcactcatgccggagggtgcaaatctcagacgact
 D L N A L M P E G C K F Q T T
 13543 gatgctttcccttcattccgcacactcgatgccggacggggactg
 D A F P S F R T L D A G R G L
 13588 gtcgttctatcttaccgaaggaggattagtcggattcgatatgctt
 V V L F T Q G G L V G F D M L
 13633 gctcgaagggtgacttatcttttcgataccaatgaggagacggct
 A R K V T Y L F D T N E E T A
 13678 tctttggattttttctcctgtggggagaccgtggtgcctatgtcaga
 S L D F S P V G D R V A Y V R
 13723 aaccataacctttacattgctcgtggagggttaaattgggagaagg
 N H N L Y I A R G G K L G E G
 13768 atgtcacgagctatcgctgtgactatcgatggaactgagactctc
 M S R A I A V T I D G T E T L
 13813 gtatatggccaggccgtacaccagcgtgaattcggtatcgaaaaa
 V Y G Q A V H Q R E F G I E K
 13858 ggtacattctggtctccaaaagggtgacctgctttctatcga
 G T F W S P K G S C L A F Y R
 13903 atggatcagagtatggtgaagcctaccccgatagtggtattatcat
 M D Q S M V K P T P I V D Y H
 13948 ccgctcgaagccgagtcctcaaacggctttattaccccatggcagg
 P L E A E S K P L Y Y P M A G
 13993 actccgtcacaccacgttacgggtgggatctatcatctggccaca
 T P S H H V T V G I Y H L A T
 14038 ggtaagaccgtctatctacaaacgggtgaacccaaggaaaaat
 G K T V Y L Q T G E P K E K F
 14083 ctgacgaatttgagttggagtccggacgaaaatatcttgatgta
 L T N L S W S P D E N I L Y V
 14128 gctgaggtgaatcgctgctcaaacgaatgtaaggtaaagtgcctat
 A E V N R A Q N E C K V N A Y
 14173 gacgctgagaccggttagattcgctccgtacgctttttgttgaaacc
 D A E T G R F V R T L F V E T
 14218 gataaacattatgtagagccgttacatccctgacattccttccg
 D K H Y V E P L H P L T F L P

Fig. 7a

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14263 ggaagtaacaatcagttcatttggcagagccgtcgcgacggatgg
G S N N Q F I W Q S R R D G W

14308 aaccatctctatctgtatgatactacaggtcgtctgatccgtcag
N H L Y L Y D T T G R L I R Q

14353 gtgacaaaaggggagtgagggttacaaactttgcaggcttcgat
V T K G E W E V T N F A G F D

14398 cccaagggaacacggctctatttcgaaagtaccgaagccagccct
P K G T R L Y F E S T E A S P

14443 ctcgaacgccatttttactgtattgatatacaaaggaggaaagaca
L E R H F Y C I D I K G G K T

14488 aaagatctgactccggagtcgggaatgcaccgcactcagctatct
K D L T P E S G M H R T Q L S

14533 cctgatggttctgccataatcgataatttttcagtcacctactgtc
P D G S A I I D I F Q S P T V

14578 ccgcgtaagggttacagtgacaaatatcggcaaagggtctcacaca
P R K V T V T N I G K G S H T

14623 ctcttgagggctaagaaccccgatacgggctatgccatgccggag
L L E A K N P D T G Y A M P E

14668 atcagaacgggtaccatcatggcgccgatgggcagacacctctt
I R T G T I M A A D G Q T P L

14713 tattacaagctcacgatgccgcttcatttcgatccggcaaagaaa
Y Y K L T M P L H F D P A K K

14758 tatcctgttattgtctatgtttacggaggacctcatgccaactc
Y P V I V Y V Y G G P H A Q L

14803 gtaaccaagacatggcgcagctctgtcgggtggatgggatattctat
V T K T W R S S V G G W D I Y

14848 atggcacagaaaggctatgccgtctttacgggtggatagtcgcgga
M A Q K G Y A V F T V D S R G

14893 tctgccaatagaggggctgctttcgagcagggtattcatcgctcgt
S A N R G A A F E Q V I H R R

14938 ttggggcagaccgagatggccgatcagatgtgcggtgtggatttc
L G Q T E M A D Q M C G V D F

14983 ctcaagagccaatcatgggtggatgccgatagaataggagtacat
L K S Q S W V D A D R I G V H

15028 ggctggagctatggtggctttatgactacgaatctgatgcttacg
G W S Y G G F M T T N L M L T

15073 cacggcgatgtcttcaaagtcggagtagccggcgggcctgtcata
H G D V F K V G V A G G P V I

15118 gactggaatcgatatgagattatgtacggtgagcgttatttcgat
D W N R Y E I M Y G E R Y F D

15163 gcgccacaggaaaatcccgaaggatacgatgctgccaacctgctc
A P Q E N P E G Y D A A N L L

15208 aaacgagccggtgatctgaaaggacgacttatgctgattcatgga
K R A G D L K G R L M L I H G

15253 gcgatcgatccggtcgtggtatggcagcattcactccttttctt

Fig. 7b

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A I D P V V V W Q H S L L F L
15298 gatgcttgcggtgaaggcacgcacctatcctgactattacgtctat
D A C V K A R T Y P D Y Y V Y
15343 ccgagccacgaacataatgtgatggggccggacagagtacatttg
P S H E H N V M G P D R V H L
15388 tatgaaacaataacccggtattttcacagatcacttatga 15426
Y E T I T R Y F T D H L *

Fig. 7c

SEQ ID NO: 38 ATGAAGAAGACAAATCTTCCAACAACATATTTCTGTCTGTGTTGTGCCCTTACAGTGGCCCTTGCCCTTGTTCGGC
TCAGTCTCCTGAAACGAGTGGTAAGGAGTTTACTCTTGAGCAACTGATGCCCGGAGGAAAGAGTTTATATA
ACTTTTACCCCGAATACGTGGTCGGTTTGCAATGGATGGAGACAATATATGTCTTTATCGAGGGTGATGAT
TTAGTTTAAATGAAGCGAATGGCAAAATCGGCTCAGACGACCAGATTTTCTGTCTGCCGATCTCAATGCACT
CATGCCGGAGGGATGCAAAATTTTCAGACGACTGATGCTTTCCCTTCAATCCGACACACTCGATGCCGGACGGG
GACTGGTCGTTCTATTTACCCAGGAGGATTAGTCGGATTCGATATGCTTGTCTGAAAGGTGACTTATCTTT
TTCGATACCAATGAGGAGACGGCTTCTTTGGATTTTCTCCTGTGGGAGACCGTGTGCTATGTCAGAAA
CCATAACCTTTACATTGCTCGTGGAGGTAAATTTGGAGAAAGGTATGTCACGAGCTATCGCTGTGACTATCG
ATGGAACGTGAGACTCTCGTATATGGCCAGGCCGTACACCGTGAATTCGGTATCGAAAGGTACATTC
TGGTCTCCAAAAGGGAGCTGCCCTTGTCTCTATCGAATGGATCAGAGTACCGGTAAAGCCCTACCCCGATAGT
GGATTATCATCCGCTCGAAGCCGAGTCCAAACCGCTTTATTAACCCCATGGCAGGTACTCCGTACACCCACG
TTACGGTTGGGATCTATCATCTGGCCACAGGTAAAGACCGTCTATCTACAAACGGGTGAACCCAAAGGAAAA
TTTCTGACGAAATTGAGTTGGAGTCCGGACGAAATATCTTGTATGTAGCTGAGGTGAATCGTGCTCAAAA
CGAATGTAAGGTAAATGCCCTATGACGCTGAGACCGGTAGATTCGTCCGTACCGCTTTTGTGTAACCGGATA
AACATTATGTAGAGCCGTACATCCCTGACATTCCTTCCGGGAAGTAACAATCAGTTCATTTTGGCAGAGC
CGTCGGACGGATGGAACCATCTCTATCTGTATGATACCTACAGGTCTGTGATCCGTACAGGTGACAAAAAGG
GGAGTGGGAGGTACAAAATTTGACGGCTTCGATCCCAAGGGAACACGGCTCTATTTCGAAAGTACCCGAG
CCAGCCCTCTCGAACGCCATTTTACTGTATTTGATATCAAGGTGCTGTGATCCGTACAGGTGACAAAAAGG
TCGGGAATGCACCCGACTCAGCTATCTCCTGATGTTCTGCCATAATCGATATTTTTCAGTCACTACTGT
CCCGCGTAAGGTTACAGTGACAAATATCGGCAAAAGGTCTCACACACTCTTGGAGGCTAAGAACCCCGATA
CGGCTATGCCATGCCGGAGATCAGAACGGGTACCATCATGGCGGCCGATGGGCAGACACCTCTTTATTAC
AAGCTACGATGCCGCTTCAATTTTCGATCCGGCAAGAGATATCCTGTTATTTGTCTATGTTTACGGAGGACC
TCATGCCCAACTCGTAACCAAGACATGGCGCAGCTCTGTCTGGATGGGATATCTATATGGCACAGAAAG
GCTATGCCGCTCTTACGGTGGATAGTCGCGGATCTGCCAATAGAGGGCTGCTTTTCGAGCAGGTTATTCTAT
CGTCGTTTGGGGCAGACCGAGATGGCCGATCAGATGTGCGGTGTGGATTTCCTCAAGAGCCCAATCATGGGT
GGATGCCGATAGAAATAGGAGTACATGGCTGGAGCTATGGTGGCTTTTATGACTACGAATCTGATGCTTACGC
ACGGCGATGCTCTCAAAGTCGGAGTAGCCCGGGGCCCTGTCTATAGACTGGAATCGATATGAGATTATGTAC
GGTGAGCGTTATTTTCGATGCCCCACAGGAAAAATCCCGAAGGATACGATGCTGCCAACCTGTCTCAACCGAGC
CGGTGATCTGAAAGGACGACTTATGCTGATTCTATGGAGCGATCGATCCGGTCTGTGGTATGGCAGCATTCAC
TCCTTTTCTTGTGATGCTTGGGTGAAGGCACGACCTATCTCTGACTATTACGTCATCTATCCGAGCCACGAAACAT
AATGTGATGGGGCCGGACAGAGTACATTTGTATGTAACAATAACCCGTTATTTTCACAGATCACTTATGA

Fig. 7d

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 00/05551

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/57 C12N9/48 A61K39/02

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X A	KIYAMA, M. ET AL.: "Sequence analysis of the Porphyromonas gingivalis dipeptidyl peptidase IV gene" BIOCHIMICA ET BIOPHYSICA ACTA, vol. 1396, no. 1, 4 March 1998 (1998-03-04), pages 39-46, XP000925951 cited in the application the whole document --- -/--	7 1-6, 8-16, 18-20

☒ Further documents are listed in the continuation of box C.

☐ Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

5 October 2000

Date of mailing of the international search report

10.01.01

Name and mailing address of the ISA

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Authorized officer

Fuchs, U

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/05551

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE WPI Section Ch, Derwent Publications Ltd., London, GB; Class B04, AN 1990-053917 XP002149298 & JP 02 005880 A (SUNSTAR KK), 10 January 1990 (1990-01-10)	7
A	abstract	1-6, 8-16, 18-20
P,X	--- BANBULA, A. ET AL.: "Prolyl Tripetidyl Peptidase from Porphyromonas gingivalis" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 274, no. 14, April 1999 (1999-04), pages 9246-9252, XP002149297 the whole document	1-16, 18-20
A	--- KABASHIMA, T. ET AL.: "Cloning, Sequencing, and Expression of the Dipeptidyl Peptidase IV Gene from Flavobacterium meningosepticum in Escherichia coli" ARCHIVES OF BIOCHEMISTRY AND BIOPHYSICS, vol. 320, no. 1, 20 June 1995 (1995-06-20), pages 123-128, XP000925965 the whole document	1-16, 18-20
A	--- KURAMITSU, H.K.: "Proteases of Porphyromonas gingivalis: what don't they do?" ORAL MICROBIOLOGY AND IMMUNOLOGY, vol. 13, no. 5, October 1998 (1998-10), pages 263-270, XP000925947 abstract page 267, column 2, line 34 -page 268, column 1, line 58 -----	1-16, 18-20

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 00/05551

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

Although claims 15 and 16 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this International application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-16 AND 18-20 COMPLETELY

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: 1-16 and 18-20 completely

An isolated prolyl tripeptidyl peptidase, active analog, active fragment, or active modification thereof having amidolytic activity for cleavage of a peptide bond present in a target polypeptide having at least 4 amino acids; an isolated prolyl tripeptidyl peptidase, active analog, active fragment, or active modification thereof being isolated from *Porphyromonas gingivalis*; an isolated polypeptide, active analog, active fragment, or active modification thereof having amidolytic activity for cleavage of a peptide bond present in a target polypeptide having at least 4 amino acids; an isolated polypeptide comprising an amino acid sequence having a percentage amino acid identity of greater than 35% with SEQ ID NO: 30; an isolated nucleic acid fragment encoding a prolyl tripeptidyl peptidase, active analog, active fragment, or active modification thereof having amidolytic activity for cleavage of a peptide bond present in a target polypeptide having at least 4 amino acids, an isolated nucleic acid fragment encoding a polypeptide comprising an amino acid sequence having a percentage amino acid identity of greater than 35% with SEQ ID NO: 30; a method of identifying an inhibitor of a prolyl tripeptidyl peptidase, active analog, active fragment, or active modification thereof; a method of reducing growth of a bacterium comprising inhibiting a prolyl tripeptidyl peptidase, active analog, active fragment, or active modification thereof; an immunogenic composition comprising an isolated prolyl tripeptidyl peptidase, or an antigenic analog, antigenic fragment, or antigenic modification thereof, the prolyl tripeptidyl peptidase having amidolytic activity for cleavage of a peptide bond present in a target peptide having at least 4 amino acids; a composition comprising an inhibitor of an isolated prolyl tripeptidyl peptidase;

2. Claim : 17 partially and 21 completely

A method of reducing growth of a bacterium comprising inhibiting a prolyl dipeptidyl peptidase, active analog, active fragment, or active modification thereof; a dipeptidyl peptidase having an amino acid sequence comprising SEQ ID NO: 43;

3. Claim : 17 partially and 22 completely

A method of reducing growth of a bacterium comprising inhibiting a prolyl dipeptidyl peptidase, active analog, active fragment, or active modification thereof; a dipeptidyl peptidase having an amino acid sequence comprising SEQ ID NO: 44;

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

4. Claim : 17 partially and 23 completely

A method of reducing growth of a bacterium comprising inhibiting a prolyl dipeptidyl peptidase, active analog, active fragment, or active modification thereof; a dipeptidyl peptidase having an amino acid sequence comprising SEQ ID NO: 45.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 00/05551

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
JP 2005880 A	10-01-1990	NONE	



PCT

[Continued on next page]

(57) Abstract: The present invention provides isolated polypeptides, prolyl tripeptidyl-peptidases, and active analogs, active fragments or active modifications thereof, having amidolytic activity for cleavage of a peptide bond present in a target peptide having at least 30 amino acids. Isolated nucleic acid fragments encoding isolated prolyl tripeptidyl-peptidases are also provided, as are methods of reducing growth of a bacterium by inhibiting a prolyl tripeptidyl-peptidase.

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BACTERIAL PROLYL PEPTIDASES AND METHODS OF USE

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CONTINUING APPLICATION DATA

This patent application claims the benefit of U.S. provisional patent application No. 60/123,148, filed March 5, 1999, which is incorporated by reference herein.

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BACKGROUND OF THE INVENTION

Porphyromonas gingivalis (formerly *Bacteroides gingivalis*) is an obligately anaerobic bacterium which is implicated in periodontal disease. *P. gingivalis* produces several distinct proteolytic enzymes, many of which are recognized as important virulence factors. A number of physiologically significant proteins, including collagen, fibronectin, immunoglobulins, complement factors C3, C4, C5, and B, lysozyme, iron-binding proteins, plasma proteinase inhibitors, fibrin and fibrinogen, and factors of the plasma coagulation cascade system, are hydrolyzed by *P. gingivalis* proteases. Broad proteolytic activity plays a role in the evasion of host defense mechanisms and the destruction of gingival connective tissue in progressive periodontitis.

Progressive periodontitis is characterized by acute tissue degradation promoted by collagen digestion and a vigorous inflammatory response characterized by excessive neutrophil infiltration. Gingival crevicular fluid accumulates in periodontitis as periodontal tissue erosion progresses at the foci of the infection, and numerous plasma proteins are exposed to proteinases expressed by the bacteria at the injury site. Neutrophils are recruited to the gingiva, in part, by the humoral chemotactic factor C5a. The complement components C3 and C5 are activated by complex plasma proteases with "trypsin-like" specificities called convertases. The human plasma convertases

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cleave the α -chains of C3 and C5 at a specific site generating biologically active factors known as anaphylatoxins (i.e. C3a and C5a). The anaphylatoxins are potent proinflammatory factors exhibiting chemotactic and/or spasmogenic activities as well as promoting increased vascular permeability. The larger products from C3 and C5 cleavage (i.e. C3b and C5b) participate in functions including complement cascade activation, opsonization, and lytic complex formation.

Recent studies have indicated that this periodontopathogen produces at least seven different enzymes belonging to the cysteine and serine catalytic classes of peptidases, among which three cysteine proteinases (gingipains) are predominant (Potempa, J., et al. (1995) *Prospect. Drug Discovery and Design* 2, 445-458). The gingipains are the best characterized group of *P. gingivalis* enzymes as their structure, function, enzymatic properties and pathological significance are known. From *in vitro* studies it is apparent that two gingipains R (also referred to generally as "Arg-gingipains" and more specifically as RgpA and RgpB), enzymes specific for cleavage at Arg-Xaa peptide bonds, have a significant potential to contribute to the development and/or maintenance of a pathological inflammatory state in infected periodontal pockets through: (i) activation of the kallikrein-kinin cascade, (ii) the release of neutrophil chemotactic activity from native and oxidized C5 of the complement pathway, and (iii) activation of factor X. In addition, gingipain K (also referred to as "Lys-gingipain"), an enzyme which cleaves Lys-Xaa peptide bonds, degrades fibrinogen. This may add to a bleeding on probing tendency associated with periodontitis. Finally, the presence of a hemagglutinin/adhesion domain in the non covalent multiprotein complexes of RgpA and gingipain K suggests participation of these enzymes in the binding of *P. gingivalis* to extracellular matrix proteins which may facilitate tissue invasion by this pathogen.

In comparison to the gingipains, relatively little is known about other cysteine proteinases produced by *P. gingivalis*. Two genes, referred to as *tp* and *prtT* have been cloned and sequenced and although they encode a putative papain-like and streptopain-like cysteine proteinases, respectively, neither has been purified and characterized.

The presence of serine proteinase activity in cultures of *P. gingivalis* has been known for several years; however, only limited information is available about such enzymes. Indeed, a serine endopeptidase has been isolated from culture media, although it was only superficially characterized (Hinode D., et al.,
5 (1993) *Infect. Immun.* 59, 3060-3068). On the other hand, an enzyme referred to as glycylprolyl peptidase (DPP IV) was found to be associated with bacterial surfaces and two molecular mass forms of this peptidase have been described. This enzyme has also been shown to possess the ability to hydrolyze partially degraded type I collagen, releasing the Gly-Pro dipeptide, and it was suggested
10 that, in collaboration with collagenase, glycylprolyl peptidase may contribute to the destruction of the periodontal ligament (Abiko, Y., et al. (1985) *J.Dent. Res.* 64, 106-111). In addition to this potential pathological function, glycylprolyl peptidase may also play a vital role in providing *P. gingivalis* with dipeptides which can be transported inside the cell and serve as a source of carbon,
15 nitrogen, and energy for this asaccharolytic organism. Recently, a gene encoding glycylprolyl peptidase in *P. gingivalis* has been cloned and sequenced, and it is now apparent that this enzyme is homologous to dipeptidyl-peptidase IV (DPP-IV) from other organisms (Kiyama, M., et al. (1998) 1396, 39-46). The nucleotide sequence of the genome of this bacterium is currently being
20 determined by The Institute for Genomic Research, and is available at www.tigr.org.

SUMMARY OF THE INVENTION

The present invention is directed to an isolated prolyl tripeptidyl-
25 peptidase, active analog, active fragment, or active modification thereof having amidolytic activity for cleavage of a peptide bond present in a target polypeptide having at least 4 amino acids. Alternatively, the isolated prolyl tripeptidyl-peptidase, active analog, active fragment, or active modification thereof is isolated from *P. gingivalis*. Typically, amidolytic activity is determined with a
30 prolyl tripeptidyl-peptidase:target polypeptide ratio of at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours. The peptide cleaved by the isolated prolyl tripeptidyl-peptidase can include the sequence of SEQ ID NO:1, SEQ ID NO:2, SEQ ID

NO:7, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:11, H-Ala-Arg-Pro-Ala-D-Lys-amide, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:25, or SEQ ID NO:37. The amino acid sequence of the isolated prolyl tripeptidyl-peptidase can include the amino acid sequence GXSEXG (SEQ ID NO:39), the amino acid sequence GXSEXG (SEQ ID NO:40), or the amino acid sequence of SEQ ID NO:30.

Another aspect of the invention is an isolated polypeptide, active analog, active fragment, or active modification thereof having amidolytic activity for cleavage of a peptide bond present in a target polypeptide having at least 4 amino acids. Typically, the polypeptide:target polypeptide ratio of at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours.

The invention is also directed to an isolated polypeptide comprising an amino acid sequence having a percentage amino acid identity of greater than 35 % with SEQ ID NO:30.

An alternative aspect of the invention is an isolated nucleic acid fragment encoding a prolyl-tripeptidyl peptidase, active analog, active fragment, or active modification thereof, having amidolytic activity for cleavage of a peptide bond present in a target polypeptide having at least 4 amino acids. Typically, the prolyl tripeptidyl-peptidase:target polypeptide ratio of at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours. The nucleic acid fragment can have a nucleotide sequence comprising SEQ ID NO:38. A complement of the nucleic acid fragment can hybridize to SEQ ID NO:38 under hybridization conditions of 0.5 M phosphate buffer, pH 7.2, 7 % SDS, 10 mM EDTA, at 68°C, followed by three for 20 minutes washes in 2x SSC, and 0.1 % SDS, at 65°C, wherein at least about 20 nucleotides of the complement hybridize.

Another aspect of the invention is an isolated nucleic acid fragment encoding a polypeptide that includes an amino acid sequence having a percentage amino acid identity of greater than 35 % with SEQ ID NO:30.

The invention is also directed at a method of identifying an inhibitor of a prolyl-tripeptidyl peptidase, active analog, active fragment, or active modification thereof, including identifying a molecule that inhibits the

amidolytic activity of the prolyl-tripeptidyl peptidase. The inhibitor is identified by incubating the prolyl-tripeptidyl peptidase with the molecule under conditions that promote amidolytic activity of the prolyl-tripeptidyl peptidase and determining if the amidolytic activity of the prolyl-tripeptidyl peptidase is inhibited relative to the amidolytic activity in the absence of molecule.

An aspect of the invention is a method of reducing growth of a bacterium. This method includes inhibiting a prolyl tripeptidyl-peptidase, active analog, active fragment, or active modification thereof, or a prolyl dipeptidyl-peptidase, active analog, active fragment, or active modification thereof. The method includes contacting the prolyl tripeptidyl-peptidase with an inhibitor of the prolyl tripeptidyl-peptidase. The method can be used to protect an animal from a periodontal disease caused by *P. gingivalis* including administering to the animal the inhibitor. The disease can be selected from the group consisting of gingivitis and periodontitis. The inhibitor can be administered by a method selected from the group consisting of subgingival application and controlled release delivery.

Another aspect of the invention is an immunogenic composition including an isolated prolyl tripeptidyl-peptidase, or an antigenic analog, antigenic fragment, or antigenic modification thereof, the prolyl tripeptidyl-peptidase having amidolytic activity for cleavage of a peptide bond present in a target peptide having at least 4 amino acids. Typically, the prolyl tripeptidyl-peptidase:target polypeptide ratio is at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours. The immunogenic composition can include an adjuvant.

The invention is also directed to a composition including an inhibitor of an isolated prolyl tripeptidyl-peptidase and a pharmaceutically acceptable carrier.

Additional aspects of the invention include a dipeptidyl peptidase having an amino acid sequence including SEQ ID NO:43, SEQ ID NO:44, or SEQ ID NO:45.

Definitions

“Polypeptide” as used herein refers to a polymer of amino acids and does not refer to a specific length of a polymer of amino acids. Thus, for example, the terms peptide, oligopeptide, protein, and enzyme are included within the definition of polypeptide. This term also includes post-expression modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations, and the like. A polypeptide can be produced by an organism, or produced using recombinant techniques, or chemically or enzymatically synthesized.

“Peptidase,” “proteinase,” and “protease” all refer to enzymes that catalyze the hydrolysis of peptide bonds in a polypeptide. A “peptide bond” or “amide bond” is a covalent bond between the alpha-amino group of one amino acid and the alpha-carboxyl group of another amino acid. “Peptidase inhibitor,” “proteinase inhibitor,” “protease inhibitor,” and “inhibitor” all refer to molecules that inhibit a peptidase that catalyzes the hydrolysis of peptide bonds in a polypeptide.

As used herein, the term “isolated” means that a polypeptide or a nucleic acid fragment has been either removed from its natural environment, produced using recombinant techniques, or chemically or enzymatically synthesized. Preferably, the polypeptide or nucleic acid fragment is purified, i.e., essentially free from any other polypeptides or nucleic acid fragments and associated cellular products or other impurities.

“Amidolytic activity” refers to the ability of a polypeptide to catalyze the hydrolysis of at least one peptide bond in a polypeptide. The term “cleavage” can also be used to refer to the hydrolysis of a peptide bond in a polypeptide. “Prolyl-tripeptidyl peptidase” and “PTP” refer to a polypeptide having a particular “amidolytic activity”. A “prolyl-tripeptidyl peptidase” is able to hydrolyze the peptide bond between the proline and the Yaa residues in a target polypeptide with the general formula $\text{NH}_2\text{-Xaa-Xaa-Pro-Yaa-(Xaa)}_n$ (SEQ ID NO:25), wherein Xaa is a natural or modified amino acid, Yaa is a natural or modified amino acid except proline, and the α -amino of the amino terminal residue is not blocked. A “prolyl tripeptidyl-peptidase” does not have to cleave all members of the target peptide. The term “natural amino acid” refers to the 20 amino acids typically produced by a cell. The term “modified amino acid”

refers to, for instance, acetylation, hydroxylation, methylation, amidation, and the attachment of carbohydrate or lipid moieties, cofactors, and the like.

A “target polypeptide” is a polypeptide that is the potential substrate of the amidolytic activity of a prolyl tripeptidyl-peptidase.

5 An active analog, active fragment, or active modification of a polypeptide of the invention is one that has amidolytic activity by hydrolysis of a peptide bond present in the target polypeptide as described herein. Active analogs, fragments, and modifications are described in greater detail herein.

10 “Nucleic acid fragment” as used herein refers to a linear polymeric form of nucleotides of any length, either ribonucleotides or deoxynucleotides, and includes both double- and single-stranded DNA and RNA. A nucleic acid fragment may include both coding and non-coding regions that can be obtained directly from a natural source (e.g., a microorganism), or can be prepared with the aid of recombinant or synthetic techniques. A nucleic acid molecule may be
15 equivalent to this nucleic acid fragment or it can include this fragment in addition to one or more other nucleotides or polynucleotides. For example, the nucleic acid molecule of the invention can be a vector, such as an expression of cloning vector.

20 “Percentage amino acid identity” refers to a comparison of the amino acids of two polypeptides as described herein.

BRIEF DESCRIPTION OF THE FIGURES

25 **Fig. 1. Purification of the prolyl tripeptidyl peptidase from the acetone precipitate of the *P. gingivalis* cell extracts. Absorbance at 280 nm (open triangles), amidolytic activity against H-Ala-Phe-Pro-pNA (closed diamonds), and H-Gly-Pro-pNA (closed circles). (a) Separation of PTP-A on hydroxyapatite. (b) Separation of PTP-A on Phenyl-Sepharose HP. (c) Separation of PTP-A on MonoQ FPLC. (d) Chromatofocusing of PTP-A on Mono-P.**

30 **Fig. 2. SDS -PAGE of fractions from purification of PTP-A and the autoradiography of the purified enzyme. Lane a, molecular mass markers (phosphorylase B, 97 kDa; bovine serum albumin, 68 kDa; ovalbumin, 43 kDa; carbonic anhydrase, 30 kDa; soybean trypsin inhibitor, 20 kDa; α -lactalbumin, 14**

kDa); *lane b*, acetone precipitate from Triton X-100 extract of *P. gingivalis*, *lane c*: hydroxyapatite column eluate; *lane d*, Phenyl-Sepharose column eluate; *lane e*, MonoQ column eluate; *lane f*, purified PTP-A from MonoP column wash; *lane g*, autoradiograph of ^3H -DFP labeled enzyme exposed for 96 h to X-ray film. All
 5 samples were reduced and boiled prior to PAGE analysis.

Fig. 3. Multiple sequence alignment of *P. gingivalis* PTP-A (PTP-A) and its bacterial and eukaryotic homologues. Pg-DPP, DPP from *P. gingivalis* (Kiyama, M., et al., (1998) *Bioch. Bioph. Acta* 1396, 39-46) containing an
 10 amino-terminal sequence corrected according to the *P. gingivalis* W83 genome data available from The Institute of Genomic Research at www.tigr.org); Fm-DPP, DPP from *Flavobacterium meningosepticum*; Hs-DPP, human DPP IV; and Mm-FAP, mouse fibroblast activation protein. Peptide sequences obtained from PTP-A analysis described herein are indicated with arrows (note that the
 15 sequence of the peptide 81-97 corresponds to the N-terminus of the lower molecular weight form of PTP-A); catalytic triad is marked with asterisks; and the proposed PTP-A membrane-anchoring N-terminal α -helix is double-underlined. Homologous regions (i.e., regions of identical amino acids and/or conservative substitutions) are highlighted. Identical regions are shown as white
 20 letters on a black background.

Fig. 4. Comparison of *P. gingivalis* PTP-A and DPP active site domains to corresponding sequences of three putative homologues identified within the *P. gingivalis* genome (DPP-H1, DPP-H2 and DPP-H3). Sequences of *P.*
 25 *gingivalis* PTP-A, DPP, DPP-H1, DPP-H2, and DPP-H3 were obtained from conceptual translation of the following open reading frames retrieved from The Institute for Genomic Research (TIGR) unfinished *P. gingivalis* genome database:
 gnl | TIGR | *P. gingivalis* contig 126 (positions 13 228 – 15 426), contig 87 (positions 6 424 – 4 399), contig 65 (positions 161 – 1 786), contig 101 (positions
 30 8 895 – 6 845), and contig 9 (positions 4 216 – 2 162), respectively. Residues predicted as catalytic triads are marked with asterisks. Homologous regions (i.e., regions of identical amino acids and/or conservative substitutions) are highlighted.

Identical regions are shown as white letters on a black background. Similar regions (i.e., conservative substitutions) are shown as white letters on a grey background.

Fig. 5. Influence of Pefabloc-serine proteinase inhibitor on *P. gingivalis* growth.

Fig. 6. Comparison of *P. gingivalis* PTP-A and DPP to sequences of three putative homologues identified within the *P. gingivalis* genome (DPP-H1, DPP-H2 and DPP-H3). Sequences of *P. gingivalis* PTP-A (126PP), DPP (87PP), DPP-H1 (65PP), DPP-H2 (101PP), and DPP-H3 (9PP) were obtained as described in Fig. 4. Homologous regions (i.e., regions of identical amino acids and/or conservative substitutions) are highlighted. Identical regions are shown as white letters on a black background. Similar regions (i.e., conservative substitutions) are shown as white letters on a grey background.

Fig. 7. Nucleotide sequence (SEQ ID NO:38) and amino acid sequence (SEQ ID NO:30) of PTP-A.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides isolated polypeptides, preferably isolated prolyl peptidases, more preferably prolyl dipeptidyl-peptidases and prolyl tripeptidyl-peptidases, most preferably prolyl-tripeptidyl peptidases, that have amidolytic activity by hydrolysis of a peptide bond present in a target polypeptide, where the bond is between a proline and an amino acid residue attached to the alpha-carboxyl group end of the proline.

When the prolyl peptidase is a prolyl tripeptidyl-peptidase, the peptidase has amidolytic activity by hydrolysis of a peptide bond present in a target polypeptide of the general formula $\text{NH}_2\text{-Xaa-Xaa-Pro-Yaa-(Xaa)}_n$ (SEQ ID NO:25), wherein Xaa is a natural or modified amino acid, Yaa is a natural or modified amino acid except proline, and the α -amino of the amino terminal residue is not blocked, wherein the peptide bond of the target polypeptide that is hydrolyzed is the Pro-Yaa peptide bond. Preferably, isolated polypeptides do not cleave a target peptide having a blocked α -amino of the amino terminal residue.

Preferably, the only peptide bond of the target peptide that is hydrolyzed is the Pro-Yaa bond. In increasing order of preference, isolated polypeptides can cleave a target peptide that is at least 4 amino acids or at least 300 Da, at least 10 amino acids or at least 750 Da, at least 20 amino acids or at least 1,500 Da, or at least 30 amino acids or at least 3,000 Da. Preferably, the prolyl-tripeptidyl peptidases cleave peptides 1, 2, 7, 8, and 10-15 shown in Table 3, human cystatin C, and interleukin 6.

When the prolyl peptidase is a prolyl dipeptidyl-peptidase, the peptidase has amidolytic activity by hydrolysis of a peptide bond present in a target polypeptide of the general formula $\text{NH}_2\text{-Xaa-Zaa-Yaa-(Xaa)}_n$ (SEQ ID NO:12), wherein Xaa is a natural or modified amino acid, Zaa is a proline or alanine, Yaa is a natural or modified amino acid except proline or hydroxyproline, and the α -amino of the amino terminal residue is not blocked, wherein the peptide bond of the target polypeptide that is hydrolyzed is the Zaa-Yaa peptide bond. Preferably, isolated polypeptides does not cleave a target peptide having a blocked α -amino of the amino terminal residue. Preferably, the only peptide bond of the target peptide that is hydrolyzed is the Pro-Yaa bond.

Due to their cyclic aliphatic character proline residues bestow unique conformational constraints on polypeptide chain structures, significantly affecting the susceptibility of proximal peptide bonds to proteolytic cleavage. Those proline residues, which often appear near the amino-termini of many biologically active peptides, may protect them against proteolytic degradation by peptidases with general specificity. A specialized group of proteolytic enzymes, typically referred to as prolyl peptidases, has evolved to cleave (i.e., hydrolyze) a peptide bond adjacent to a proline residue in a polypeptide. The peptide bond adjacent to a proline residue can be referred to as a prolyl-X bond, where prolyl is the proline residue, and X is an amino acid residue attached to the alpha-carboxyl group end of the proline. The bacterial prolyl peptidases can cleave a polypeptide to liberate a tripeptide or a dipeptide. Prolyl peptidases that do not cleave a target peptide if the α -amino of the amino terminal residue is blocked can be referred to as exopeptidases. The *in vivo* activity of these specialized proteolytic enzymes may have important physiological significance, because it may lead to inactivation of many biologically active peptides and/or transformation of the activity of other

biologically active peptides. In addition, hydrolysis of prolyl-X bonds in conjunction with general catabolic pathways should allow the complete re-utilization of amino acids by living organisms, including bacteria. However, prolyl peptidases from bacterial pathogens, if released into the host environment, may interfere with the physiological functions of biologically active polypeptides and, therefore, contribute to the pathogenicity of infectious disease.

The external (i.e., cell surface) localization and uncontrolled activity of bacterial peptidases, including prolyl peptidases, likely contributes significantly to run-away inflammation in the human host and the pathological degradation of connective tissue during periodontitis. For instance, working in concert bacterial prolyl peptidases (e.g., prolyl tripeptidyl peptidases and DPP IV) have the ability to completely degrade collagen fragments locally generated by endogenous or bacterial collagenases. Because type I collagen is the major component of periodontal ligament, its enhanced degradation by bacterial prolyl peptidases may contribute to loss of tooth attachment and periodontal pocket formation. Thus, there is a need in the art to characterize bacterial peptidases to facilitate the development of therapies to inhibit the activity of the bacterial peptidases.

The polypeptides of the present invention, preferably prolyl peptidases, can be used as a source of antibodies for inhibiting the peptidase activity and thereby possibly reducing periodontitis, loss of tooth attachment and periodontal pocket formation. Antibodies to prolyl peptidases can also be used to identify and/or isolate additional prolyl peptidases. Knowledge of prolyl peptidases can also be used to make inhibitors of prolyl peptidases and to make immunogenic compositions that could be used to elicit the production of antibodies to prolyl peptidases and thereby possibly reduce gingivitis, periodontitis, loss of tooth attachment, and/or periodontal pocket formation.

An example of a prolyl-tripeptidyl peptidase is prolyl-tripeptidyl peptidase A (SEQ ID NO:30) (also referred to as PTP-A) from *P. gingivalis*. Purified PTP-A has apparent molecular masses of 81.8 and 75.8 kDa. The lower molecular mass peptidase may be due to the proteolytic cleavage of the peptidase from the surface of *P. gingivalis*. PTP-A is a new member of clan SC, family S9 of serine peptidases. Clans of serine peptidases are grouped on the basis of the order of certain amino acids in the polypeptide that make up the "catalytic triad" which

plays a pivotal role peptidase activity. The members of the clan SC are characterized by the catalytic triad in the polypeptide in the order of serine, aspartic acid, and histidine. Members of the clan SC are also characterized by a tertiary structure including $\beta/\alpha/\beta$ units, and an α/β hydrolase fold. In addition to the catalytic triad order, the amino acid sequence GXSEXG (SEQ ID NO:39), where X is any amino acid and S is the active site serine, is a signature of all members of the clan SC with some distinguishing features specific for each family. Family S9 has the consensus sequence GXSEXG (SEQ ID NO:40). Besides this consensus sequence, there is a general similarity of primary structures which classifies peptidases to this family. For instance, peptidases of this family generally have two domains, an amino-terminal domain that contains a membrane binding domain, and a carboxy-terminal domain, also referred to as the catalytic domain. The catalytic domain contains the residues of the catalytic triad. Some members of the S9 family have only the catalytic domain.

The S9 family is diverged and divided in three subfamilies: S9A, cytosolic oligopeptidases from archae and eukaryotes; S9B, eukaryotic acylaminoacylpeptidases; and S9C, dipeptidyl peptidase IV from bacteria and eukaryotes. The catalytic domain of peptidases from family S9 typically begin at about residue 400 of SEQ ID NO:30 and include the remaining carboxy-terminal amino acids (see, e.g., Fulop, et al., (1998) *Cell* 94, 161-170). Despite structural similarities to peptidases from the S9 family, the tripeptidyl-peptidase activity of PTP-A is unusual for this family of enzymes, and no other known similar activity has so far been attributed to any other member of the S9 family. In fact, all strict tripeptidyl-peptidases belong only to the subtilisin family (S8) and S33 family of serine peptidases; however, they neither share a structural relationship with PTP-A nor have activity limited to cleavage after proline residues. In particular, there are no other known prolyl tripeptidyl peptidases with an activity that is increased by iodoacetamide relative to the same prolyl tripeptidyl peptidase in the absence of iodoacetamide under the same conditions. Iodoacetamide is a compound that is traditionally a peptidase inhibitor. Typically, the activity of a prolyl tripeptidyl peptidase is increased about two-fold. Furthermore, unlike oligopeptidases, the prolyl tripeptidyl-peptidases of the present invention can cleave target peptides having as few as 4 amino acids but also target peptides having at least 30 amino

acids or a molecular weight of at least 3,000 Da. In these respects, the *P. gingivalis* tripeptidyl peptidase is a unique enzyme, and the isolation and characterization of this novel bacterial prolyl peptidase will facilitate the development of therapies to inhibit the activity of the bacterial peptidases.

5 Examples of putative prolyl-dipeptidyl peptidases are DPP-H1 (SEQ ID NO:43), DPP-H2 (SEQ ID NO:44), and DPP-H3 (SEQ ID NO:45). These peptidases have a significant percentage amino acid similarity with DPP IV and PTP-A (see Fig. 6). Each dipeptidyl peptidase is expected to have enzymatic activity, as each has a well preserved catalytic triad (Fig. 4). DPP IV has been
10 characterized and the gene encoding the peptidase has been cloned, however the substrate specificity has not been well characterized. DPP IV has been found to cleave SEQ ID NOs:6, 20, 23, and 24. DPP IV has been purified in two forms. One of the forms is a full length gene translation product containing a blocked amino-terminal residue. The second form had the amino-terminal amino acid
15 sequence HSYRAAVYDYDVRRLVKPLSEHVG (SEQ ID NO:48), which corresponds to residues 116-140 of DPP IV (Kiyama, M., et al. (1998) 1396, 39-46), indicating that it was proteolytically truncated on the amino-terminus.

 In *P. gingivalis*, PTP-A and DPP IV activity is cell surface associated. While not intending to be limiting, it is conceivable that the enzyme is membrane
20 anchored through a putative signal sequence which is not cleaved but remains as a membrane spanning domain similar to other members of the prolyl oligopeptidase family. However, a significant portion of the purified PTP-A has a truncated N-terminus, apparently due to cleavage by Lys-specific peptidase and likely to be an artifact which has occurred during the purification procedure. Nevertheless,
25 membrane bound PTP-A and DPP IV is proteolytically cleaved and shed during cultivation of the bacteria, as indicated by variable amount of soluble activities found in cell free culture media. The cell surface localization of PTP-A supports a putative physiological function in providing nutrients for growing bacterial cells. The inability of asaccharolytic *P. gingivalis* to utilize free amino acids makes the
30 bacterium entirely dependant on an external peptide supply. In this regard, PTP-A and DPP IV activities are probably very important, if not indispensable, for bacterial growth, and inhibition of prolyl tripeptidyl-peptidases and dipeptidyl-peptidases may inhibit the *in vivo* growth of organisms, including *P. gingivalis*.

For instance, treatment of *P. gingivalis* cultures in lagphase (i.e., the period after inoculation of a culture and before the organism begins to divide) and early logarithmic growth with the inhibitors PEFABLOCK and 3,4-dichloroisocoumarin inhibits growth of *P. gingivalis*.

5 Preferably, a polypeptide of the invention, preferably a prolyl peptidase, contains the amino acid sequence GXSEXG (SEQ ID NO:39), most preferably, GXSEXGG (SEQ ID NO:40), where G is glycine, X is any amino acid, and S is the active site serine. The active site serine can be identified by, for instance, labeling with diisopropylfluorophosphate as described herein. Preferably, the catalytic
10 domain of the prolyl tripeptidyl-peptidases of the invention begins at about residue 400 of SEQ ID NO:30 and includes the remaining carboxy-terminal amino acids and the corresponding amino acids of SEQ ID NOs:43-45 (see Fig. 6), more preferably, at about residue 502 of SEQ ID NO:30 and includes the remaining carboxy-terminal amino acids and the corresponding amino acids of SEQ ID
15 NOs:43-45 (see Fig. 6), most preferably, at about residue 556 of SEQ ID NO:30 and includes the remaining carboxy-terminal amino acids and the corresponding amino acids of SEQ ID NOs:43-45 (see Fig. 6).

 The invention further includes a polypeptide, preferably a prolyl tripeptidyl-peptidase, that shares a significant level of primary structure with SEQ ID NO:30.
20 The two amino acid sequences (i.e., the amino acid sequence of the polypeptide and the sequence SEQ ID NO:30) are aligned such that the residues that make up the catalytic triad, i.e., the serine, aspartic acid, and the histidine, are in register, then further aligned to maximize the number of amino acids that they have in common along the lengths of their sequences; gaps in either or both sequences are permitted
25 in making the alignment in order to place the residues of the catalytic triad in register and to maximize the number of shared amino acids, although the amino acids in each sequence must nonetheless remain in their proper order. The percentage amino acid identity is the higher of the following two numbers: (a) the number of amino acids that the two sequences have in common within the
30 alignment, divided by the number of amino acids in SEQ ID NO:30, multiplied by 100; or (b) the number of amino acids that the two sequences have in common within the alignment, divided by the number of amino acids in the candidate polypeptide, multiplied by 100. Preferably, a prolyl tripeptidyl peptidase has

greater than 35 % identity, more preferably at least about 40 % identity, most preferably at least about 45 % identity with SEQ ID NO:30. Preferably, amino acids 154-732 of SEQ ID NO:30 are used, more preferably amino acids 400-732 of SEQ ID NO:30 are used. An isolated polypeptide comprising an amino acid
5 sequence having a percentage amino acid identity of greater than 35 % with SEQ ID NO:30.

In general, the amidolytic activity of the polypeptides of the invention, preferably prolyl peptidases, can be measured by assay of the cleavage of a target polypeptide in the presence of prolyl peptidase and a buffer. Preferably, the lower
10 ratio of prolyl tripeptidyl-peptidase to target polypeptide is at least about 1:1, more preferably at least about 1:100, even more preferably at least about 1:1,000, most preferably at least about 1:10,000. Preferably, the higher ratio of prolyl peptidase to target polypeptide is no greater than about 1:10,000,000, more preferably no greater than about 1:1,000,000 and most preferably no greater than about
15 1:100,000. Buffers in which a prolyl peptidase is active are suitable for the assay. Preferably, the buffer is about 200 mM HEPES (N-2-hydroxyethylpiperazine,N'-2-ethansulfonic acid), more preferably about 50 mM HEPES, most preferably about 20 mM HEPES. Preferably, the pH of the buffer is at least about pH 6.0 and no greater than pH 8.0, more preferably about pH 7.5. Preferably, the temperature of
20 the assay is at about 37°C. The assay can be carried out for at least about 1 minute to no greater than 24 hours. Preferably, the amidolytic activity of the prolyl peptidases are measured at a prolyl peptidase:target polypeptide ratio of at least about 1:100 to no greater than 1:1,000,000 in about 200 mM HEPES, about pH 7.5 at about 37°C for at least about 3 hours. In general, the time of the assay can vary
25 depending on the substrate and enzyme:substrate ratio. Typically, target peptides are stable under these conditions, and typically it is difficult to detect background levels of hydrolysis in the absence of a prolyl peptidase. Preferably, the assay is allowed to continue until at least 1 % of the target peptide is hydrolyzed.

Prolyl-tripeptidyl peptidases of the present invention preferably are
30 inhibited by a compound chosen from the group consisting of PEFABLOCK (4-(2-aminoethyl)-benzenesulfonyl-fluoride hydrochloride), diisopropylfluorophosphate, and 3,4-dichloroisocoumarin, more preferably PEFABLOCK and diisopropylfluorophosphate, and most preferably diisopropylfluorophosphate. The

peptidases of the present invention are preferably not inhibited by a compound chosen from the group consisting of leupeptin, antipain, E-64, pepstatin, α_1 -proteinase inhibitor, α_1 -antichymotrypsin and α_2 -macroglobulin, most preferably. Significantly and unexpectedly, the amidolytic activity of a prolyl-tripeptidyl
5 peptidase of the present invention is increased by iodoacetamide relative to the prolyl-tripeptidyl peptidase in the absence of iodoacetamide under the same conditions. Preferably, the effect of iodoacetamide on amidolytic activity is measured by incubating in 200 mM HEPES, pH 7.6, at least about 0.1 nM of the prolyl tripeptidyl-peptidase with the inhibitor for about 15 minutes, adding about 1
10 mM of H-Ala-Phe-Pro-pHA, and incubating for at least about 1 minute before assaying for amidolytic activity. Typically, at least about 1 mM to no greater than 100 mM of inhibitor is used.

The polypeptides of the invention include a polypeptide having SEQ ID NO:30, or an active analog, active fragment, or active modification of SEQ ID
15 NO:30. An active analog, active fragment, or active modification of a polypeptide having SEQ ID NO:30 is one that has amidolytic activity by hydrolysis of the Pro-Yaa peptide bond present in a target polypeptide of the general formula $\text{NH}_2\text{-Xaa-Xaa-Pro-Yaa-(Xaa)}_n$ (SEQ ID NO:25). Active analogs of a polypeptide having SEQ ID NO:30 include prolyl-tripeptidyl peptidases having amino acid
20 substitutions that do not eliminate hydrolysis of SEQ ID NO:25 at the Pro-Yaa peptide bond. Substitutes for an amino acid may be selected from other members of the class to which the amino acid belongs. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and tyrosine. Polar neutral amino acids include glycine, serine,
25 threonine, cysteine, tyrosine, asparagine and glutamine. The positively charged (basic) amino acids include arginine, lysine and histidine. The negatively charged (acidic) amino acids include aspartic acid and glutamic acid. Examples of preferred conservative substitutions include Lys for Arg and *vice versa* to maintain a positive charge; Glu for Asp and *vice versa* to maintain a negative charge; Ser for
30 Thr so that a free -OH is maintained; and Gln for Asn to maintain a free NH_2 .

Active fragments of a prolyl-tripeptidyl peptidase of the invention include prolyl-tripeptidyl peptidases containing deletions or additions of one or more contiguous or noncontiguous amino acids such that the resulting polypeptide will

hydrolyze SEQ ID NO:25 at the Pro-Yaa peptide bond. An example of a fragment of a prolyl-tripeptidyl peptidase is a catalytic domain. Modified prolyl-tripeptidyl peptidases include prolyl-tripeptidyl peptidases that are chemically and enzymatically derivatized at one or more constituent amino acid, including side chain modifications, backbone modifications, and N- and C- terminal modifications including acetylation, hydroxylation, methylation, amidation, and the attachment of carbohydrate or lipid moieties, cofactors, and the like. Modified prolyl-tripeptidyl peptidases will hydrolyze SEQ ID NO:25 at the Pro-Yaa peptide bond.

Prolyl peptidases can be obtained by several methods. Isolation of a prolyl-tripeptidyl peptidase present on the surface of a cell producing the peptidase typically requires lysis of the cell followed by purification methods that are well known in the art. Alternatively, cells can be treated with a detergent, for instance Triton X-100, to remove the peptidase from the cell surface. The following are nonlimiting examples of suitable protein purification procedures: fractionation on immunoaffinity, ion-exchange, hydroxyapatite, Phenyl-Sepharose HP, MonoQ HR 5/5, or MonoP columns; ethanol precipitation; reverse phase HPLC; chromatography on silica or on an ion-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75. Preferably, isolation of a prolyl-tripeptidyl peptidase from *P. gingivalis* is accomplished using a combination of hydroxyapatite, Phenyl-Sepharose HP, MonoQ HR 5/5 and MonoP column chromatography steps as described herein.

Prolyl peptidases can also be isolated from organisms other than *P. gingivalis*. Other organisms can express a prolyl-tripeptidyl peptidase that is encoded by a coding region having similarity to the PTP-A coding region. A "coding region" is a linear form of nucleotides that encodes a polypeptide, usually via mRNA, when placed under the control of appropriate regulatory sequences. The boundaries of a coding region are generally determined by a translation start codon at its 5' end and a translation stop codon at its 3' end. "Regulatory region" refers to a nucleic acid fragment that regulates expression of a coding region to which a regulatory region is operably linked. Non limiting examples of regulatory regions include promoters, transcription initiation sites, translation start sites, translation

stop sites, and terminators. "Operably linked" refers to a juxtaposition wherein the components so described are in a relationship permitting them to function in their intended manner. A regulatory element is "operably linked" to a coding region when it is joined in such a way that expression of the coding region is achieved under conditions compatible with the regulatory region. Alternatively, other organisms can express a prolyl-tripeptidyl peptidase from a recombinant coding region encoding the peptidase. The identification of similar coding regions in other organisms can be accomplished as described herein. A prolyl-tripeptidyl peptidase can be isolated using purification methods that are well known in the art.

Alternatively, the peptidase can be chemically synthesized using methods that are well known in the art including, for instance, solid phase synthesis. Examples of, for instance, coding and regulatory regions are described herein.

The expression of a prolyl-tripeptidyl peptidase by an organism other than *P. gingivalis* can be detected using specific substrates of the general formula $\text{NH}_2\text{-Xaa-Xaa-Pro-LG}$ or $\text{NH}_2\text{-Xaa-Xaa-Pro-Yaa}$ (SEQ ID NO:41), where LG is a leaving group. The leaving group can be a chromogenic or fluorogenic group known to the art. The expression of a prolyl-tripeptidyl peptidase by an organism and subsequent cleavage of a specific substrate results in a free amino acid or a free leaving group, each of which can be assayed using techniques known to those of skill in the art. Other methods can be based on immunogenic properties of PTP-A, for instance immunoassays and histochemistry, the detection of mRNA, and PCR related methods, all of which are known to one of skill in the art.

As described in the Examples, the amino acid sequence of the amino-terminal end of a PTP-A fragment was used to identify the nucleotide sequence of the PTP coding region. The nucleotide sequence was present in a publically available database containing the nucleotide sequence of the partially finished *P. gingivalis* W83 genome. However, even though the nucleotides that encode the *P. gingivalis* PTP-A were known, there was no indication that the nucleotides were in fact transcribed and translated. The data obtained from the database only contained the nucleotide sequence of a genomic clone; there was no disclosure that the nucleotides did or did not contain an open reading frame. Moreover, there is little data known to the art regarding regulatory regions required for either the transcription or the translation of a nucleotide sequence in *P. gingivalis*.

Thus, a person of ordinary skill, having the nucleotide sequence of the genomic clone, would not be able to predict that the open reading frame encoding PTP-A was transcribed or translated. Moreover, even if there was a suggestion that the open reading frame was both transcribed and translated, there is no suggestion
5 that the polypeptide encoded by the open reading frame would have the novel activity of PTP-A.

Accordingly, the present invention is directed to a nucleic acid fragment encoding a polypeptide, particularly a prolyl-tripeptidyl peptidase, active analog, active fragment, or active modification thereof. The nucleic acid fragment can
10 have a nucleotide sequence as shown in SEQ ID NO:38. Alternatively, nucleic acid fragments of the invention include those whose complement hybridize to SEQ ID NO:38 under standard hybridization conditions as described herein. During hybridization the entire nucleotide sequence of the complement can hybridize with SEQ ID NO:38. Preferably, at least about 20 nucleotides of the complement
15 hybridize with SEQ ID NO:38, more preferably at least about 50 nucleotides, most preferably at least about 100 nucleotides.

Alternatively, the nucleic acid fragment can have a nucleotide sequence encoding a polypeptide having the amino acid sequence shown in SEQ ID NO:30. An example of the class of nucleotide sequences encoding such a polypeptide is
20 SEQ ID NO:38. This class of nucleotide sequences is large but finite, and the nucleotide sequence of each member of the class can be readily determined by one skilled in the art by reference to the standard genetic code.

The identification of similar coding regions in other organisms can be accomplished by screening individual wild-type microorganisms for the presence
25 of nucleotide sequences that are similar to the coding region of PTP-A, which is shown in SEQ ID NO:38. Screening methods include, for instance, hybridization of a detectably labeled probe with a nucleic acid fragment.

Standard hybridizing conditions are a modification of the conditions used by Church et al. ((1984) *Proc. Natl. Acad. Sci. USA* 81, 1991): 0.5 M phosphate
30 buffer, pH 7.2, 7 % SDS, 10 mM EDTA, at 68°C, and three washes, each for 20 minutes in 2x SSC, 0.1 % SDS, at 65°C. Preferably, a probe will hybridize to the nucleotide sequence set forth in SEQ ID NO:38 under standard hybridizing conditions. Generally the probe does not have to be complementary to all the

nucleotides of the nucleic acid fragment as long as there is hybridization under the above-stated conditions.

“Complement” and “complementary” refer to the ability of two single stranded nucleic acid fragments to base pair with each other, where an adenine on one nucleic acid fragment will base pair to a thymine on a second nucleic acid fragment and a cytosine on one nucleic acid fragment will base pair to a guanine on a second nucleic acid fragment. Two nucleic acid fragments are complementary to each other when a nucleotide sequence in one nucleic acid fragment can base pair with a nucleotide sequence in a second nucleic acid fragment. For instance, 5'-ATGC and 5'-GCAT are complementary. The term complement and complementary also encompasses two nucleic acid fragments where one nucleic acid fragment contains at least one nucleotide that will not base pair to at least one nucleotide present on a second nucleic acid fragment. For instance the third nucleotide of each of the two nucleic acid fragments 5'-ATTGC and 5'-GCTAT will not base pair, but these two nucleic acid fragments are complementary as defined herein. Typically two nucleic acid fragments are complementary if they hybridize under the standard conditions referred to herein.

Preferred probes are nucleic acid fragments complementary to a coding region or another nucleotide sequence that encodes a prolyl-tripeptidyl peptidase. For instance, a probe can comprise a consecutive series of nucleotides complementary to a portion of SEQ ID NO:38. Preferably a probe is at least about 18 bases, more preferably at least about 21 bases, and most preferably at least about 24 bases in length. Particularly preferred probes are TTCGATCCGGCAAAGAAATATCCTGTTATTGTCTATGTTTACGGAGGAC CT (SEQ ID NO:36, GTGGATGCCGATAGAATAGGAGTACATGGCTGGAGCTATGGTGGCTTT (SEQ ID NO:37, and SEQ ID NO:38. Methods of detectably labeling a probe are well known to the art.

The nucleic acid fragment that is identified by the probe is further analyzed to determine if it encodes a polypeptide with amidolytic activity of the Pro-Yaa

peptide bond on a target polypeptide of the general formula $\text{NH}_2\text{-Xaa-Xaa-Pro-Yaa-(Xaa)}_n$ (SEQ ID NO:25). Another method for screening individual microorganisms for the presence of nucleotide sequences that are similar to the coding regions of the present invention is the polymerase chain reaction (PCR).

5 Individual wild-type microorganisms containing nucleic acid fragments encoding a prolyl-tripeptidyl peptidase can also be identified using antibody. Preferably the antibody is directed to PTP-A. The production of antibodies to a particular polypeptide is known to a person of skill in the art, and is further detailed herein.

10 The use of hybridization of a probe to a coding region present in individual wild-type microorganisms can be used as a method to identify a coding region identical or similar to a coding region present in SEQ ID NO:38. The coding region can then be isolated and ligated into a vector as described below. Two nucleic acid sequences are "similar" if the two nucleic acid sequences can be aligned so that the number of identical amino acids along the lengths of their sequences are optimized. 15 Preferably, two nucleotide acid sequences have, in increasing order of preference, preferably at least about 90 %, at least about 92 %, at least about 94%, at least about 96%, most preferably at least about 98% identity.

As mentioned above, a nucleic acid fragment of the invention can be 20 inserted in a vector. Construction of vectors containing a nucleic acid fragment of the invention employs standard ligation techniques known in the art. See, e.g., Sambrook et al, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press (1989) or Ausubel, R.M., ed. *Current Protocols in Molecular Biology* (1994). A vector can provide for further cloning (amplification of the 25 nucleic acid fragment), i.e., a cloning vector, or for expression of the polypeptide encoded by the coding region, i.e., an expression vector. The term vector includes, but is not limited to, plasmid vectors, viral vectors, cosmid vectors, or artificial chromosome vectors. Typically, a vector is capable of replication in a bacterial host, for instance *E. coli*. Preferably the vector is a plasmid.

30 Selection of a vector depends upon a variety of desired characteristics in the resulting construct, such as a selection marker, vector replication rate, and the like. Suitable plasmids for expression in *E. coli*, for example, include pUC(X), pKK223-3, pKK223-2, pTrc99A, and pET-(X) wherein (X) denotes a vector family in which

numerous constructs are available. pUC(X) vectors can be obtained from Pharmacia Biotech (Piscataway, NH) or Sigma Chemical Co. (St. Louis, MO). pKK223-3, pKK233-2 and pTrc99A can be obtained from Pharmacia Biotech. pET-(X) vectors can be obtained from Promega (Madison, WI) Stratagene (La Jolla, CA) and Novagen (Madison, WI). To facilitate replication inside a host cell, the vector preferably includes an origin of replication (known as an "ori") or replicon. For example, ColE1 and P15A replicons are commonly used in plasmids that are to be propagated in *E. coli*.

An expression vector optionally includes regulatory regions operably linked to the coding region. The invention is not limited by the use of any particular promoter, and a wide variety are known. Promoters act as regulatory signals that bind RNA polymerase in a cell to initiate transcription of a downstream (3' direction) coding region. The promoter used in the invention can be a constitutive or an inducible promoter. It can be, but need not be, heterologous with respect to the host cell. Preferred promoters for bacterial transformation include *lac*, *lacUV5*, *tac*, *trc*, T7, SP6 and *ara*.

An expression vector can optionally include a Shine Dalgarno site (e.g., a ribosome binding site), and a start site (e.g., the codon ATG) to initiate translation of the transcribed message to produce the enzyme. It can also include a termination sequence to end translation. A termination sequence is typically a codon for which there exists no corresponding aminoacyl-tRNA, thus ending polypeptide synthesis. The nucleic acid fragment used to transform the host cell can optionally further include a transcription termination sequence. The *rrnB* terminators, which is a stretch of DNA that contains two terminators, T1 and T2, is an often used terminator that is incorporated into bacterial expression systems (J. Brosius et al., (1981) *J. Mol. Biol.* 148 107-127).

The nucleic acid fragment used to transform the host cell optionally includes one or more marker sequences, which typically encode a polypeptide that inactivates or otherwise detects or is detected by a compound in the growth medium. For example, the inclusion of a marker sequence can render the transformed cell resistant to an antibiotic, or it can confer compound-specific metabolism on the transformed cell. Examples of a marker sequence are sequences that confer resistance to kanamycin, ampicillin, chloramphenicol, and tetracycline.

Antibodies can be produced to a polypeptide having the sequence of SEQ ID NOs:30, 43, 44 or 45, or a polypeptide having a percentage amino acid identity as described herein. Alternatively, antibodies can be made to an antigenic analog, antigenic fragment, or antigenic modification of a polypeptide having the sequence of SEQ ID NOs:30, 43, 44 or 45. An antigenic analog, antigenic fragment, or antigenic modification of a polypeptide having SEQ ID NOs:30, 43, 44 or 45 is one that generates an immune response in an animal. Antigenic analogs of a polypeptide having SEQ ID NOs:30, 43, 44 or 45 include prolyl peptidases having amino acid substitutions that do not eliminate peptide antigenicity in an animal. Substitutes for an amino acid may be selected from other members of the class to which the amino acid belongs, as described herein. Fragments of a prolyl peptidase of the invention include prolyl peptidases containing deletions or additions of one or more contiguous or noncontiguous amino acids such that the resulting polypeptide will generate an immune response in an animal. An example of a fragments of a prolylpeptidase is a catalytic domain. Modified prolyl peptidases include prolyl peptidases that are chemically and enzymatically derivatized at one or more constituent amino acids, including side chain modifications, backbone modifications, and N- and C- terminal modifications including acetylation, hydroxylation, methylation, amidation, and the attachment of carbohydrate or lipid moieties, cofactors, and the like.

Accordingly, an aspect of the invention is an immunogenic composition comprising an isolated prolyl peptidase, or an antigenic analog, antigenic fragment, or antigenic modification thereof, preferably a prolyl tripeptidyl-peptidase. The prolyl tripeptidyl-peptidase preferably has amidolytic activity for cleavage of the Pro-Yaa peptide bond present in a target polypeptide with the general formula $\text{NH}_2\text{-Xaa-Xaa-Pro-Yaa-(Xaa)}_n$ (SEQ ID NO:25), wherein the amidolytic activity is measured at a prolyl tripeptidyl-peptidase:target polypeptide ratio of at least about 1:100 to no greater than about 1:1,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours.

The immunogenic composition can further include excipients or diluents that are pharmaceutically acceptable as carriers and compatible with the immunogenic composition. The term "pharmaceutically acceptable carrier" refers to a carrier(s) that is "acceptable" in the sense of being compatible with the other

ingredients of a composition and not deleterious to the recipient thereof. Suitable excipients are, for example, water, saline, dextrose, glycerol, ethanol, or the like, and combinations thereof. In addition, if desired, the immunogenic composition may contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents, and/or adjuvants which enhance the effectiveness of the immune-stimulating composition.

The immunogenic composition can be used in a method for protecting an animal from a disease caused by *P. gingivalis*. This method includes administering the immunogenic composition and eliciting antibodies to a prolyl peptidase, antigenic analog, antigenic fragment, or antigenic modification. The diseases that can be treated in this manner include periodontal diseases, which includes gingivitis and periodontitis. Clinical hallmarks of periodontitis include loss of tooth attachment and periodontal pocket formation.

Alternatively and preferably, periodontal diseases can be treated by the use of inhibitors of a prolyl peptidase. An inhibitor of a prolyl peptidase, preferably a prolyl tripeptidyl-peptidase, can be present in a composition that preferably contains a pharmaceutically acceptable carrier. For instance, inhibitors can be applied systemically, subgingivally (e.g., subgingival irrigation) and/or by controlled release delivery directly into the periodontal pocket using methods well known to the art (see, e.g., Kornman, K., (1993) *J. Periodontol.* 64, 782-791). Preferably, an inhibitor is applied subgingivally or by controlled release delivery.

The prolyl peptidases, active analogs, fragments, and modifications thereof can be used in a method of reducing growth of bacteria *in vitro* or *in vivo*. Preferably, the bacteria is a periodontal pathogen, i.e., a bacterial pathogen that causes periodontal disease, more preferably the bacteria is *P. gingivalis*. The inability of asaccharolytic *P. gingivalis* to utilize free amino acids makes the bacterium entirely dependant on an external peptide supply. The action of the polypeptides of the invention may be required for bacterial growth, and inhibition of the polypeptides of the invention may inhibit the *in vivo* growth of organisms, including *P. gingivalis*. The method includes decreasing the amount of dipeptides and/or tripeptides (e.g., the result of cleavage of SEQ ID NO:25 by a prolyl-tripeptidyl peptidase) and the amount of free amino acids that result from further cleavage of the dipeptides and/or tripeptides present by inhibiting a prolyl

peptidase, active analog, active fragment, or active modification thereof, such that the amount of dipeptides and/or tripeptides generated by the polypeptides is decreased. The amount of dipeptides and/or tripeptides is decreased relative to the amount of dipeptides and/or tripeptides present in the absence of the inhibitor.

5 Preferably, the amount of dipeptides and/or tripeptides generated is decreased by an inhibitor, a monoclonal antibody that inhibits the prolyl peptidase, or polyclonal antibodies that inhibit the prolyl peptidase, more preferably, the amount of dipeptides and/or tripeptides generated is decreased by an inhibitor. Preferably, an inhibitor acts to inhibit a polypeptide of the invention, preferably a prolyl peptidase,
10 by blocking the active site of the polypeptide. The polypeptide can be present on the surface of the bacteria or secreted into the environment, preferably the polypeptide is present in the surface of the bacteria.

The present invention is also directed to a method of developing an inhibitor of a prolyl peptidase, active analog, active fragment, or active
15 modification thereof, preferably a prolyl-tripeptidyl peptidase. The method includes identifying a molecule that inhibits the amidolytic activity of the prolyl peptidase. This can be accomplished by, for instance, incubating the prolyl peptidase with a candidate molecule under conditions that promote amidolytic activity of the prolyl peptidase and determining if the amidolytic activity of the
20 prolyl peptidase is decreased relative to the amidolytic activity in the absence of the molecule. The amidolytic activity can be measured by cleavage of the Pro-Yaa peptide bond present in the target polypeptide SEQ ID NO:25 as described herein. One method of developing an inhibitor includes using the target peptide SEQ ID NO:25 and replacing the Xaa residues with modified amino acids. It is expected
25 that some modified amino acids will cause the target peptide to act as an inhibitor.

EXAMPLES

The present invention is illustrated by the following examples. It is to be understood that the particular examples, materials, amounts, and procedures are to
30 be interpreted broadly in accordance with the scope and spirit of the invention as set forth herein.

Example 1

Materials

Diisopropylfluorophosphate (DFP), leupeptin and 3,4-dichloroisocoumarin, were purchased from Calbiochem (La Jolla, CA). Antipain, iodoacetamide, substance P, bradykinin and bradykinin related peptides, were obtained from Sigma. Other peptides used in this study were synthesized at the Molecular Genetic Instrumental Facility (University of Georgia, Athens, GA) using Fmoc protocol with an advanced ChemTech MPS350 automated synthesizer. H-Ala-Phe-Pro-pNA, H-Gly-Pro-pNA, Z-Gly-Pro-pNA, Z-Ala-Pro-pNA, and H-Pro-pNA (where pNA is p- Nitroanilide; Z is benzyloxycarbonyl; and H is hydrogen and denotes an unblocked amino-terminal group) were obtained from Bachem (King of Prussia, PA). Prolinal was kindly provided by Dr. James Powers (Georgia Institute of Technology, Atlanta) and cystatin C by Dr. Magnus Abrahamson (University of Lund, Sweden).

Methods

Source and Cultivation of Bacteria— *P. gingivalis* HG66 was obtained from Dr. Roland Arnold (University of North Carolina, Chapel Hill), while the strains W50 (ATCC 53978) and ATCC 33277 were obtained from the ATCC. All cells were grown as described previously (Chen, Z., et al., (1992) *J. Biol. Chem.* 267, 18896-18901).

Enzyme Activity Assays— Routinely, the tripeptidyl peptidase amidolytic activity was measured with H-Ala-Phe-Pro-pNA (1mM) in 0.2 M HEPES (N-2-hydroxyethylpiperazine,N'-2-ethansulfonic acid), pH 7.5 at 37°C. The concentration of enzyme was 0.1 nM to 1 nM. The assay was performed in a total volume of 0.2 ml on microplates, and the initial turnover rate was recorded at 405 nm using a microplate reader (Spectramax Molecular Devices, Sunnyvale, CA). In inhibition studies, the enzyme was first preincubated with inhibitor for 15 min at 37°C, substrate added, and residual activity recorded after 5 minutes to 30 minutes. H-Gly-Pro-pNA, Z-Ala-Pro-pNA, Z-Gly-Pro-pNA and H-Pro-pNA (1 mM final concentration) were assayed in the same manner.

Protein Determination—Protein concentration was determined using the BCA reagent kit (Sigma, St. Louis, MO), using bovine serum albumin as a standard.

Localization of Tripeptidyl-Peptidase Activity—Cultures of *P. gingivalis* HG66, W50 and ATCC 33277, at different phases of growth, were subjected to the following fractionation procedure. The cells were removed by centrifugation (10,000 x g, 30 minutes), washed twice with 10 mM Tris, 150 mM NaCl, pH 7.4, resuspended in 50 mM Tris, pH 7.6, and disintegrated by ultrasonication in an ice bath at 1500 Hz for 5 cycles (5 minutes sonication/5 minutes brake). Unbroken cells and large debris were removed by centrifugation (10,000 x g, 30 minutes) and the opalescent supernatant subjected to ultracentrifugation (150,000 x g, 120 minutes), yielding a pellet containing bacterial membranes and a supernatant which was considered as membrane-free cell extract. All fractions, as well as the full culture, culture medium, and full culture after sonication, were assayed for amidolytic activity against H-Ala-Phe-Pro-pNA.

Enzyme Purification—All purification steps were performed at 4°C except for FPLC separations, which were carried out at room temperature. Cells were harvested by centrifugation (6,000 x g, 30 minutes), washed with 50 mM potassium phosphate buffer, pH 7.4, and resuspended in the same buffer (150 ml per 50 gram of cells wet weight). Triton X-100 (10% volume/volume in H₂O) was added slowly to the bacterial cell suspension to a final concentration of 0.05%. After 120 minutes of gentle stirring, unbroken cells were removed by centrifugation (28,000 x g, 60 minutes). Proteins in the supernatant were precipitated with cold acetone (-20°C) added to a final concentration of 60% and collected by centrifugation. The pellet was redissolved in 50 mM potassium phosphate buffer, pH 7.0, and extensively dialyzed against 20 mM potassium phosphate, pH 7.0, containing 0.02% sodium azide. The dialyzed fraction was clarified by centrifugation (28,000 x g, 30 min) and applied to a hydroxyapatite column (BioRad, Melville, NY) equilibrated with 20 mM potassium phosphate, pH 7.0, at a flow rate of 20 ml/hour. After equilibration, the column was washed until the A₂₈₀ fell to zero. Bound proteins were eluted with a gradient from 20-300 mM potassium phosphate and fractions (7 ml) analyzed for dipeptidyl- and tripeptidyl-peptidase activity using H-Gly-Pro-pNA and H-Ala-Phe-Pro-pNA, respectively. The activity against the latter

substrate was pooled, saturated with 1 M ammonium sulfate, clarified by centrifugation, and directly loaded onto a Phenyl-Sepharose HP (Pharmacia, Piscataway, NJ) column equilibrated with 50 mM potassium phosphate, pH 7.0, containing 1 M ammonium sulfate. The column was washed with two volumes of equilibration buffer, followed by buffer containing 0.5 M ammonium sulfate, and developed with a descending gradient of ammonium sulfate from 0.5 to 0 M. Active fractions were pooled, extensively dialyzed against 20 mM Tris, pH 7.5, and applied to a MonoQ HR 5/5 FPLC column equilibrated with the same buffer. The column was washed with 5 volumes of equilibration buffer at 1.0 ml/minute, following which bound proteins were eluted with a gradient of 0- 300 mM NaCl. The active fractions were pooled, dialyzed against 25 mM Bis-Tris, pH 6.3, and subjected to chromatofocusing on a MonoP FPLC column equilibrated with Bis-Tris buffer, using a pH gradient developed with 50 ml of 10x diluted Polybuffer 74 (Pharmacia), adjusted to a pH of 4.0.

Electrophoretic Techniques—The SDS-PAGE system of Schagger and von Jagow (Schagger, H., and von Jagow, G. (1987) *Anal. Biochem.* 166, 368-379), was used to monitor enzyme purification and estimate the enzyme molecular mass. For amino-terminal sequence analysis, proteins resolved in SDS-PAGE were electroblotted to polyvinylidene difluoride membranes using 10 mM CAPS, pH 11, 10% methanol (Matsudaira, P. (1987) *J. Biol. Chem.* 262, 10035-10038). The membrane was washed thoroughly with water and stained with Coomassie Blue G250. The blot was air dried, and protein bands cut out and subjected to NH₂-terminal sequence analysis with an Applied Biosystems 491 Protein Sequencer using the program designed by the manufacturers.

Enzyme Fragmentation—The purified prolyl tripeptidyl peptidase (PTP-A) was partially denatured by incubation in 6 M urea in 0.02 M Tris, pH 7.6, for 60 minutes. Low molecular mass gingipain R (RgpB) (Potempa, J., et al. (1995) *Prospect. Drug Discovery and Design* 2, 445-458) from *P. gingivalis* was then added to make an enzyme:substrate molar ratio of 1:100. The reaction mixture was made in 1 mM cysteine and the sample incubated overnight at 37°C. Generated peptides were separated by reverse-phase HPLC using a μ Bondapak C-18 column (3.9 x 300 mm) (Waters, Millford, MA). Peptides were eluted with 0.1% trifluoroacetic acid and acetonitrile containing 0.08% trifluoroacetic acid, using a

gradient from 0 to 80% acetonitrile over 60 minutes. Peptides were monitored at 220 nm and collected manually.

For determination of the active site serine residue and to confirm that the purified enzyme was a serine peptidase, 100 µg of purified PTP-A was first
5 incubated with 170 µCi of [1,3-³H]DFP (Amersham, Arlington Heights, IL) for 30 minutes at 25°C in 20 mM HEPES, pH 7.5. The reaction was quenched by addition of cold DFP to a final concentration of 10 mM and the radiolabelled material analyzed by SDS-PAGE, followed by autoradiographic analysis. The gel was dehydrated, soaked in PPO solution for 2 hours, dried, and the DFP-binding
10 proteins detected by fluorography after an exposure time of 96 hours on X-ray film (XAR; Kodak, Rochester, NY). The bulk of radiolabelled protein was subjected to proteolytic fragmentation with RgpB and peptides obtained separated by reverse-phase HPLC as described above. Radioactivity in each peptide fraction was measured using a β liquid scintillation counter, and the labeled peptide, as well as
15 other selected peptides were subjected to sequence analysis.

Identification of the PTP-A Gene— The database containing the unfinished *P. gingivalis* W83 genome, available from The Institute for Genomic Research, was searched for the presence of nucleotide sequences corresponding to the NH₂-terminal and the internal PTP-A amino acid sequences using the TBLASTN
20 algorithm, BLAST version 2.0.8, and the default values for all parameters (Altschul, S.F., et al., (1997) *Nucleic Acid Res.* 25, 3389-3402). An identified clone gnl | TIGR | *P. gingivalis*_126 was retrieved from The Institute for Genomic Research data base (<http://www.tigr.org>). The position of the PTP-A gene was localized using the NCBI open reading frame (ORF) finder (available from the
25 National Center for Biotechnology Information, at <http://www.ncbi.nlm.nih.gov/gorf/gorf.html>). The amino acid sequence, obtained by conceptual translation of the entire ORF, was further used for homology screening by use of the NCBI BLAST search tool.

Enzyme Specificity— Peptides were incubated with 1 µg PTP-A at an
30 enzyme:substrate molar ratio of 1:100 for 3 hours or 24 hours in 50 µl of 200 mM HEPES, pH 7.5, at 37°C, and the reaction stopped by acidification with trifluoroacetic acid. The samples were then subjected to reverse-phase high

pressure liquid chromatography using a μ Bondapak C-18 column (3.9 x 300 mm) (Waters, Millford, MA) and an acetonitrile gradient (0-80 % in 0.075% trifluoroacetic acid in 50 min). Each peak, detected at 220 nm, was collected, lyophilized, re-dissolved in 50% (volume/volume) methanol, 0.1% acetic acid and subjected to analysis by mass spectrometry.

Mass Spectrometry—A Finnigan MAT 95S, sector mass spectrometer (Finnigan MAT, Bremen, Germany) equipped with an electrospray source (ESI) was used operated essentially as described previously (Stenfors, C., et al., (1997) *J. Biol. Chem.* 272, 5747-5751). Peptides were identified by fitting of the obtained spectra to specific sequences using an Internet application program MsFit available at <http://falcon.ludwig.ucl.ac.uk/msfit.html>.

Example 2

Enzyme Localization, Purification and Initial Characterization

Analysis of amidolytic activity against H-Ala-Phe-Pro-pNA in several fractions of *P. gingivalis* HG66, W50 and ATCC 33277 clearly indicated that an enzyme(s) with prolyl tripeptidyl-peptidase activity is localized on the cell surface in all strains tested with less than 5% of the total activity being found in the medium regardless of the growth phase of the bacterial culture. Cell associated enzyme was easily detached from the bacterial surface by treatment with a low concentration (0.05%) of Triton X-100. This procedure released more than 85-90% of activity in a soluble form. Subsequent acetone precipitation of proteins in the Triton X-100 fraction successfully separated the activity from pigment which remained in solution. The redissolved protein fraction, after dialysis, was applied to hydroxyapatite (100 ml) equilibrated with 20 mM potassium phosphate buffer pH 7.0. The elution was carried out with 20 mM potassium phosphate buffer pH 7.0, using a phosphate gradient from 20 mM to 300 mM at flow rate 20 ml/h. At this step substantial separation of the PTP-A activity from both the DPP IV and bulk protein was achieved (Fig. 1a). Further purification performed by subsequent chromatography steps including Phenyl-Sepharose (Fig. 1b), MonoQ (Fig. 1c) and MonoP columns (Fig. 1d), resulted in the isolation of purified enzyme.

Phenyl-Sepharose HP (25 ml) was equilibrated with 50 mM potassium phosphate, 1M ammonium sulfate, pH 7.0, at flow rate 30 ml/h. The column was

washed with two volumes of equilibration buffer and a step gradient of 0.5 M ammonium sulfate was applied, following which a descending gradient of 0.5 to 0 M ammonium sulfate was applied. The PTP-A containing fractions were extensively dialyzed against 20 mM Tris-HCl, pH 7.0, and concentrated by ultrafiltration. The concentrated PTP-A containing fractions were applied to a MonoQ column equilibrated with the same buffer. The column was washed with 5 volumes of equilibration buffer, following which bound protein was eluted with a gradient of 0-300 mM NaCl. The concentrated fraction of PTP-A from the MonoQ column was equilibrated with 25 mM Bis-Tris, pH 6.3, and loaded on a MonoP column equilibrated with the same buffer. A pH gradient was developed using 50 ml of Polybuffer 74, with the pH adjusted to 4.0.

Significantly, the chromatography step on the MonoP column yielded the A_{280} profile much sharper than the activity peak. Although this imperfect overlap of protein and activity may suggest that the protein component does not represent the active enzyme, the rest of data argues with such a contention. This apparent contradiction may be likely explained by the enzyme inhibition by the reaction product of H-Ala-Phe-Pro-pNA hydrolysis but this possibility has not been explored. The yield of protein and activity recovery in a typical purification procedure is summarized in Table 1.

Table 1. Purification of the PTP- A from *P. gingivalis*

Step	Volume (ml)	Protein (mg)	Total activity*	Specific activity (units/mg)	Purification fold	Yield (%)
5	Triton X-100 extract after centrifugation					
	200	1200	757 673	642	1	100
	Acetone precipitate					
10	50	600	537 622	896	1.4	71
	Hydroxyapatite chromatography					
	50	22	400 039	18 183	28	53
15	Phenyl-Sepharose					
	48	10	312 505	31 250	48	41
	3	1.5	244 828	163 218	254	32
MonoQ						
MonoP						
	4	0.7	188 400	269 142	420	25

* Based on the enzymatic activity using H-Ala-Phe-Pro-pNA where one unit = mOD/min/1ml

SDS-PAGE analysis of the purified enzyme revealed the presence of two protein bands with apparent molecular masses of 81.8 and 75.8 kDa, respectively (Fig. 2, lane f). Autoradiography of the enzyme sample radiolabeled with [1,3-³H]DFP (Fig. 2, lane g) clearly indicated that the bands represented either two distinct serine peptidases or different molecular mass forms of the same enzyme. In an attempt to distinguish between these two options, the electrophoretically resolved proteins were subjected to amino terminal sequence analysis. Unfortunately, it was found that the 81.8 kDa form of PTP-A had a blocked N-terminus. In contrast, the sequence NH₂-SAQTTRFSAADLNALMP (SEQ ID NO:23) was found at the N-terminus of the lower molecular mass form of the enzyme. This result led us to the possibility that the 75.8 kDa form of PTP-A was derived from the 81.8 kDa form through proteolytic cleavage of a 6 kDa amino-terminal peptide. To confirm this hypothesis and, in addition, to localize the active site residue within *P. gingivalis* PTP-A, the mixture containing both radiolabeled enzymes was proteolytically fragmented and peptides resolved by reverse-phase HPLC. This procedure yielded only one major radioactive peptide peak, and the purified peptide was found to have a single amino acid sequence: IGVHGWXYGGFMTTNL (SEQ ID NO:24), where X apparently represents the active-site serine residue covalently and irreversibly modified by DFP. These data convincingly indicate that the two protein bands of purified PTP-A represents different forms of the same enzyme. The portion of the purified PTP-A having a truncated N-terminus may be due to cleavage by Lys-specific peptidase and is likely to be an artifact which occurred during the purification procedure. Nevertheless, the proteolytic shedding of membrane bound PTP-A also occurs during cultivation of the bacteria, as indicated by variable amount of soluble activities found in cell free culture media.

Example 3

pH Optimum, Stability and Inhibition Profile

Using the amidolytic activity assay with H-Ala-Phe-Pro-pNA it was found that the enzyme has a broad pH optimum from pH 6.0 to 8.0 and in 0.2 M HEPES, pH 7.6 was stable for at least 12 hours at 25°C or 37°C. PTP-A activity was not affected by class specific synthetic inhibitors of cysteine or metalloproteinases

(Table 2). In contrast, preincubation of the enzyme with DFP or PEFABLOCK resulted in total loss of activity, supporting its classification as a serine peptidase. Surprisingly, however, 3,4-dichloroisocoumarin was only a poor inhibitor, and PMSF, leupeptin, antipain and prolinal had no effect at all. Interestingly, preincubation of PTP-A with iodoacetamide, but not with N-ethylmaleimide, stimulated enzyme amidolytic activity about two-fold. Human plasma inhibitors, such as α_1 -proteinase inhibitor, α_1 -antichymotrypsin and α_2 -macroglobulin did not affect the enzyme activity, nor were they cleaved by PTP-A.

The effect of inhibitors on amidolytic activity of DPP IV was also determined using the same conditions as those used for PTP-A, but using H-Gly-Pro-pNA as a substrate.

Table 2. Effect of inhibitors on the amidolytic activity of PTP-A and DPP IV.
Results are for a 15-min incubation at 37 C in 0.2 HEPES pH 7.6,
with 1 mM H-Ala-Phe-Pro-pNA as substrate.

	Inhibitor	Concentration	Residual activity of PTP-A, %	Residual activity of DPP IV, %
5	Diisopropyl fluorophosphate	10 mM	0	0
		10 mM	96	20
10	Phenylmethanesulfonyl fluoride	1mg/ml	20	15
		10mg/ml	0	0
	PEFABLOC SC	1 mM	56	100
15	3,4-dichloroisocoumarin	5mM	200	100
	Iodoacetamide	5 mM	100	100
	N-Ethylmaleimide	1 mM	98	100
20	1,10- orthophenanthroline	5 mM	93	100
		0.1 mM	100	100
	EDTA	0.1 mM	100	100
25	Leupeptin	0.1 mM	100	20
	Antipain	10 mM	100	0
30	Prolinal	10 mM	100	30
	Val-Pro	10 mM	100	1
	Ala-Pro			
35	Ala-Gly-Pro			

Example 4

Substrate Specificity

Among several chromogenic substrates tested, including H-Ala-Phe-Pro-pNA, H-Gly-Pro-pNA, Z-Gly-Pro-pNA, Z-Ala-Pro-pNA, H-Pro-pNA, only H-Ala-Phe-Pro-pNA was hydrolyzed by PTP-A indicating a prolyl specific tripeptidyl-peptidase activity. To further confirm this specificity several synthetic peptides composed of 5 to 34 amino acid residues and containing at least one proline residue were tested as substrates for PTP-A. Out of 22 peptides tested only those with a proline residue in the third position from the amino terminal end were cleaved (Table 3), with the significant exception of peptides with adjacent proline residues (peptides 3, 4 and 16). In addition, a free α -amino group was absolutely required for cleavage after the third proline residue as exemplified by resistance to enzymatic hydrolysis of peptide 9, which differs from the peptide 8 only in acylation of the α -amino group of the N-terminal valine residue. Except for these two limitations, the peptide bond -Pro-↓-Yaa- was cleaved at the same rate in all peptides with the general formula $\text{NH}_2\text{-Xaa-Xaa-Pro-Yaa-(Xaa)}_n$ (SEQ ID NO:25), where Xaa represents any amino acid residue while Yaa could be any residue except proline, regardless of the chemical nature of the amino acids and the length of the peptide. In all cases the reaction was completed within 3 hours and prolonged incubation for 24 hours did not affect the pattern of cleavage, confirming the absolute requirement for a proline residue at the third position from the unblocked N-terminus. In addition, these data indicate that the preparation of PTP-A was free of any contamination with either aminopeptidase, dipeptidyl peptidase, or endopeptidase activities.

The cleavage specificity of DPP IV was also determined using the same conditions as those used for PTP-A. The results (Table 3) demonstrate that DPP IV does not cleave between two proline residues.

Table 3. Cleavage specificity of PTP-A and DPP IV on synthetic peptides.

Substrate	Cleavage site	SEQ ID NO:
Peptide 1	H-Arg-Pro-Pro- -Gly-Phe-Ser-Pro-Phe-Arg	1
Peptide 2	H-Arg-Pro-Pro- -Gly-Phe	2
Peptide 3	H-Lys-Arg-Pro-Pro-Gly-Phe-Ser-Pro-Phe-Arg	3
Peptide 4	H-Tyr-Arg-Pro-Pro-Gly-Phe-Ser-Pro-Phe-Arg	4
Peptide 5	H-Arg-Pro-Hyp-Gly-Phe-Ser-Pro-Phe-Arg	5
Peptide 6	H-Arg-Pro- -Lys-Pro- -Gln-Gln-Phe-Phe-Gly-Leu-Met-NH ₂	6
Peptide 7	H-Val-Pro-Pro- -Gly-Glu-Asp-Ser-Lys-Glu-Val-Ala-Ala-Pro-His-Arg-Gln	7
Peptide 8	H-Val-Pro-Pro- -Gly-Glu-Asp-Ser-Lys	8
Peptide 9	Ac-Val-Pro-Pro-Gly-Glu-Asp-Ser-Lys	9
Peptide 10	H-Val-Glu-Pro- -Ile-Pro-Tyr	10
Peptide 11	H-Arg-Gly-Pro- -Phe-Pro-Ile	11
Peptide 12	H-Ala-Arg-Pro- -Ala-D-Lys-amide	13
Peptide 13	H-Pro-Asn-Pro- -Asn-Gln-Gly-Asn-Phe-Ile	14
Peptide 14	H-Arg-His-Pro- -Lys-Tyr-Lys-Thr-Glu-Leu	15
Peptide 15	H-Gly-Val-Pro- -Lys-Thr-His-Leu-Glu-Leu	16
Peptide 16	H-Lys-Gly-Pro-Pro-Ala-Ala-Leu-Thr-Leu	17
Peptide 17	H-Gln-Lys-Gln-Met-Ser-Asp-Arg-Glu-Asn-Asp-Met-Ser-Pro-Ser-Asn-Val-Val-Pro-Ile-His-Val-Pro-Pro-Thr-Thr-Glu-Asn-Lys-Pro-Lys-Val-Gln	18
Peptide 18	H-Phe-Leu-Arg-Glu-Pro-Val-Ile-Phe-Leu	19
Peptide 19	H-Gly-Ile-Arg-Pro-Tyr-Glu-Ile-Leu-Ala	20
Peptide 20	H-Leu-Pro- -Asp-Leu-Asp-Ser-Ser-Leu-Ala-Ser-Ile-Gln-Glu-Leu-Ser-Pro-Gln-Glu-Pro-Arg-Pro-Pro-Glu-Ala	21
Peptide 21	H-Cys-Leu-Ser-Ser-Gly-Thr-Leu-Pro-Gly-Pro-Gly-Asn-Asp-Ala-Ser-Arg-Glu-Leu-Glu-Ser	22
Peptide 22	H-Lys-Ile-Ala-Gly-Tyr-His-Leu-Glu-Leu	46
Peptide 23	H-Ser-Pro- -Tyr-Ser-Ser-Asp-Thr-Thr	47
Peptide 24	H-Ala-Pro- -Val-Arg-Ser-Leu-Asn-Cys-Thr-Leu-Arg-Asp-Ser-Gln-Gln-Lys	

| indicates cleavage site mediated by PTP-A

† indicates cleavage site mediated by DPP IV

The lack of cleavage after internal proline residues in the synthetic peptides corresponds well with the absence of any proteolytic activity on several protein substrates including IgA, IgG, albumin, azocasein, carboxymethylated ribonuclease and gelatin. However, the size of substrate, which is a limiting factor in the activity of oligopeptidases (Walter, R., et al., (1980) *Mol. Cell. Biochem.* 30, 111-126), is not restricting in the case of PTP-A, because the enzyme is able to cleave a tripeptide (NH₂-Xaa-Xaa-Pro) from the N-terminus of both human cystatin C and interleukin 6.

Example 5

PTP-A Sequence Analysis

Partial PTP-A amino acid sequence data allowed us to identify the *P. gingivalis* genomic clone gnl | TIGR | *P. gingivalis*_126 in the Unfinished Microbial Genomes data base, TIGR. An ORF corresponding to the PTP-A amino acid sequence was found as indicated by the fact that all sequences of the PTP-A derived peptides obtained by the enzyme polypeptide fragmentation with RgpB were present in the protein primary structure inferred from the nucleotide sequence of the ORF. The 732 amino acid polypeptide with a calculated mass of 82, 266 Da was encoded in this ORF. The homology search performed using the NCBI TBLASTN tool against GenBank+EMBL+DDBJ+PDB databases and subsequent multiple sequence alignments using the ClustalW Multiple Sequence Alignment tool (Fig. 3) indicated that PTP-A is a new member of the prolyl oligopeptidase (S9) family of serine peptidases (Rawlings, N.D., et al., (1991) *Biochem. J.* 279, 907-908).

The sequence GX SXGG (SEQ ID NO:40) is a signature feature for the S9 family of serine peptidases. Within this large and diverse S9 family of evolutionary and functionally related enzymes both from prokaryotes and eukaryotes, PTP-A was most closely related to bacterial dipeptidyl peptidase IV (DPP IV) from *Flavobacterium meningosepticum*, *Xantomonas maltophilus*, and *P. gingivalis*, sharing 31.6%, 30.4%, and 28.5% amino acid sequence identity, respectively. Remarkably, the COOH-terminal region of the PTP-A molecule (residues 502 - 732) shows a significant similarity to the eukaryotic prolyl oligopeptidases with 34% and 33% identity to human DPP IV and mouse fibroblast activation protein (FAP), respectively (Fig. 3). This part of the molecule contains the amino acid

residues which encompass the catalytic triad in all characterized prolyl oligopeptidases, and from the multiple alignments with DPP IV of confirmed active site residues (Kabashima, T., et al., (1995) *Arch. Biochem. Biophys.* 320, 123-128) it is apparent that Ser-603, Asp-678 and His-710 represent the catalytic triad of PTP-A (Fig. 3). Such an inference is further supported by the direct labeling of Ser-603 by DFP. In addition, the computer assisted search for sequential motifs characteristic for transmembrane domains revealed the presence of such a putative region within the N-terminal sequences of PTP-A, with residues 5 to 25 most likely folded into a hydrophobic α -helix responsible for membrane anchoring of this enzyme.

In *P. gingivalis* PTP-A, as well as in DPP IV, all activities are cell surface associated, and it is conceivable that the enzymes are membrane anchored through putative signal sequences which are not cleaved but remain as a membrane spanning domain similar to other members of the prolyl oligopeptidase family. The cell surface localization of di- and tripeptidyl-peptidases suggests a putative physiological function in providing nutrients for growing bacterial cells. Here, the inability of asaccharolytic *P. gingivalis* to utilize free amino acids (Dashper, S.G., et al., *J. Dent Res.* 77, 1133 (Abstract) (1988)) makes the bacterium entirely dependant on an external peptide supply. In this regard, DPP-IV and PTP-A activities are probably very important, if not indispensable, for bacterial growth.

This suggestion is strongly corroborated by the fact that the *P. gingivalis* genome contains three additional genes encoding peptidases homologous with DPP-IV and PTP-A and one related to aminopeptidase B. The peptidases homologous with DPP-IV and PTP-A are referred to as homologs H1 (SEQ ID NO:43), H2 (SEQ ID NO:44), and H3 (SEQ ID NO:45) (Fig. 6). If expressed, each gene product would probably have enzymatic activity because each has a well preserved catalytic triad (Fig. 4). In addition, all of these genes encode a putative signal peptide which may act in providing membrane-anchorage motifs.

Example 6**Influence of Proteinase Inhibitor on *P. gingivalis* Growth**

To evaluate whether *P. gingivalis* growth was influenced by the presence of a peptidase inhibitor, *P. gingivalis* in logphase growth was diluted 1:5 into liquid media and incubated at 37°C. The cell density was monitored by measuring the optical density at 600 nm (OD₆₀₀). When the optical density began to increase, Pefabloc was added at 0.5 mg/ml or at 2.0 mg/ml. The control culture received no Pefabloc. The cultures receiving Pefabloc exhibited decreased growth (Figure 5). The peptidase inhibitor had to be added before the culture reached an OD₆₀₀ of about 0.3 for the peptidase inhibitor to have an effect on growth.

The complete disclosures of all patents, patent applications, publications, and nucleic acid and protein database entries, including for example GenBank accession numbers and EMBL accession numbers, that are cited herein are hereby incorporated by reference as if individually incorporated. Various modifications and alterations of this invention will become apparent to those skilled in the art without departing from the scope and spirit of this invention, and it should be understood that this invention is not to be unduly limited to the illustrative embodiments set forth herein.

Sequence Listing Free Text

- SEQ ID NOs:1-11: Synthetic peptides
- SEQ ID NO:12: Target peptide
- SEQ ID NOs:13-22: Synthetic peptides
- SEQ ID NO:23: Amino-terminus of the lower molecular mass form of PTP-A.
- SEQ ID NO:24: Amino acid sequence present in PTP-A, where X apparently represents the active-site serine residue covalently and irreversibly modified by DFP.
- SEQ ID NO:25: Target peptide, where Xaa represents a natural or modified amino acid residue, Yaa represents a natural or modified amino acid residue except proline, and N is equal to or greater than 1.
- SEQ ID NO:26: Mouse fibroblast activation protein

	SEQ ID NO:27:	Human DPP IV
	SEQ ID NO:28:	DPP from <i>Flavobacterium meningosepticum</i>
	SEQ ID NO:29:	DPP from <i>P. gingivalis</i>
	SEQ ID NO:30:	<i>P. gingivalis</i> PTP-A
5	SEQ ID NO:31:	Portion of PTP-A
	SEQ ID NO:32:	Portion of DPP from <i>P. gingivalis</i>
	SEQ ID NO:33:	Portion of H1 homolog of <i>P. gingivalis</i> DPP
	SEQ ID NO:34:	Portion of H2 homolog of <i>P. gingivalis</i> DPP
	SEQ ID NO:35:	Portion of H3 homolog of <i>P. gingivalis</i> DPP
10	SEQ ID NOs:36-37:	Probes
	SEQ ID NO:38:	Nucleotide sequence of coding region encoding PTP-A.
	SEQ ID NO:39:	Consensus sequence for clan SC where X is any amino acid and S is the active site serine GXSTXXG.
	SEQ ID NO:40:	Consensus sequence for family S9 where X is any amino acid and S is the active site serine GXSTXGG.
15	SEQ ID NO:41:	A specific substrate for a prolyl-tripeptidyl peptidase, where Xaa represents a natural or modified amino acid residue, and Yaa represents a natural or modified amino acid residue except proline.
20	SEQ ID NO:42:	DPP from <i>P. gingivalis</i>
	SEQ ID NO:43:	H1 homolog of <i>P. gingivalis</i> DPP
	SEQ ID NO:44:	H2 homolog of <i>P. gingivalis</i> DPP
	SEQ ID NO:45:	H3 homolog of <i>P. gingivalis</i> DPP
	SEQ ID NO:46:	Synthetic peptides
25	SEQ ID NO:47:	Synthetic peptides
	SEQ ID NO:48:	Amino terminal sequence of DPP IV

What is claimed is:

1. An isolated prolyl tripeptidyl-peptidase, active analog, active fragment, or active modification thereof having amidolytic activity for cleavage of a peptide bond present in a target polypeptide having at least 4 amino acids, wherein the prolyl tripeptidyl-peptidase:target polypeptide ratio is at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours.
2. An isolated prolyl tripeptidyl-peptidase, active analog, active fragment, or active modification thereof having amidolytic activity at a prolyl tripeptidyl-peptidase:target polypeptide ratio of at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours, and wherein the prolyl tripeptidyl-peptidase is isolated from *P. gingivalis*.
3. The isolated prolyl tripeptidyl-peptidase of claim 2 wherein the peptide cleaved by the isolated prolyl tripeptidyl-peptidase comprises the sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:11, H-Ala-Arg-Pro-Ala-D-Lys-amide, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:25, and SEQ ID NO:37.
4. The isolated prolyl tripeptidyl-peptidase of claim 2 wherein the amino acid sequence of the isolated prolyl tripeptidyl-peptidase comprises the amino acid sequence GXSEXG (SEQ ID NO:39).
5. The isolated prolyl tripeptidyl-peptidase of claim 4 wherein the amino acid sequence of the isolated prolyl tripeptidyl-peptidase comprises the amino acid sequence GXSEXG (SEQ ID NO:40).
6. The isolated prolyl tripeptidyl-peptidase of claim 4 wherein the amino acid sequence of the isolated prolyl tripeptidyl-peptidase comprises SEQ ID NO:30.

7. An isolated polypeptide, active analog, active fragment, or active modification thereof having amidolytic activity for cleavage of a peptide bond present in a target polypeptide having at least 4 amino acids, wherein the polypeptide:target polypeptide ratio of at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours.
8. An isolated polypeptide comprising an amino acid sequence having a percentage amino acid identity of greater than 35 % with SEQ ID NO:30.
9. An isolated nucleic acid fragment encoding a prolyl-tripeptidyl peptidase, active analog, active fragment, or active modification thereof, having amidolytic activity for cleavage of a peptide bond present in a target polypeptide having at least 4 amino acids, wherein the prolyl tripeptidyl-peptidase:target polypeptide ratio of at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours.
10. The nucleic acid fragment of claim 9 wherein the nucleic acid fragment has a nucleotide sequence comprising SEQ ID NO:38.
11. The nucleic acid fragment of claim 9 wherein a complement of the nucleic acid fragment hybridizes to SEQ ID NO:38 under hybridization conditions of 0.5 M phosphate buffer, pH 7.2, 7 % SDS, 10 mM EDTA, at 68°C, followed by three for 20 minutes washes in 2x SSC, and 0.1 % SDS, at 65°C, wherein at least about 20 nucleotides of the complement hybridize.
12. An isolated nucleic acid fragment encoding a polypeptide wherein the polypeptide comprises an amino acid sequence having a percentage amino acid identity of greater than 35 % with SEQ ID NO:30.
13. A method of identifying an inhibitor of a prolyl-tripeptidyl peptidase, active analog, active fragment, or active modification thereof, comprising identifying a molecule that inhibits the amidolytic activity of the prolyl-

tripeptidyl peptidase by incubating the prolyl-tripeptidyl peptidase with the molecule under conditions that promote amidolytic activity of the prolyl-tripeptidyl peptidase and determining if the amidolytic activity of the prolyl-tripeptidyl peptidase is inhibited relative to the amidolytic activity in the absence of molecule.

14. A method of reducing growth of a bacterium comprising inhibiting a prolyl tripeptidyl-peptidase, active analog, active fragment, or active modification thereof, by contacting the prolyl tripeptidyl-peptidase with an inhibitor of the prolyl tripeptidyl-peptidase.
15. A method for protecting an animal from a periodontal disease caused by *P. gingivalis* comprising administering to the animal the inhibitor of claim 14 wherein the disease is selected from the group consisting of gingivitis and periodontitis.
16. The method of claim 15 wherein the inhibitor is administered by a method selected from the group consisting of subgingival application and controlled release delivery.
17. A method of reducing growth of a bacterium comprising inhibiting a prolyl dipeptidyl-peptidase, active analog, active fragment, or active modification thereof, by contacting the prolyl dipeptidyl-peptidase with an inhibitor of the prolyl dipeptidyl-peptidase.
18. An immunogenic composition comprising an isolated prolyl tripeptidyl-peptidase, or an antigenic analog, antigenic fragment, or antigenic modification thereof, the prolyl tripeptidyl-peptidase having amidolytic activity for cleavage of a peptide bond present in a target peptide having at least 4 amino acids, wherein the prolyl tripeptidyl-peptidase:target polypeptide ratio is at least about 1:1 to no greater than about 1:10,000,000 in about 200 mM HEPES, about pH 7.5 at 37°C for at least about 3 hours.
19. The immunogenic composition of claim 18 further comprising an adjuvant.

20. A composition comprising an inhibitor of an isolated prolyl tripeptidyl-peptidase and a pharmaceutically acceptable carrier.
21. A dipeptidyl peptidase having an amino acid sequence comprising SEQ ID NO:43.
22. A dipeptidyl peptidase having an amino acid sequence comprising SEQ ID NO:44.
23. A dipeptidyl peptidase having an amino acid sequence comprising SEQ ID NO:45.

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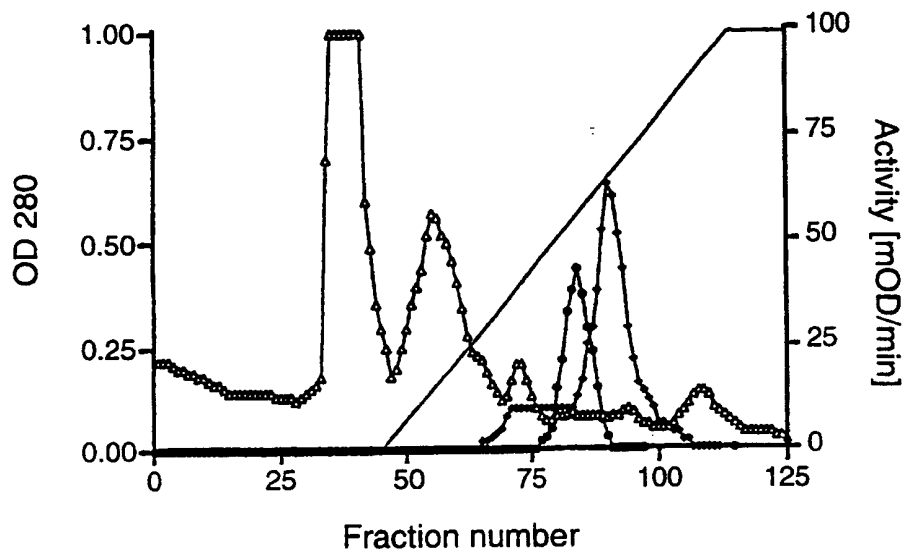


Fig. 1a

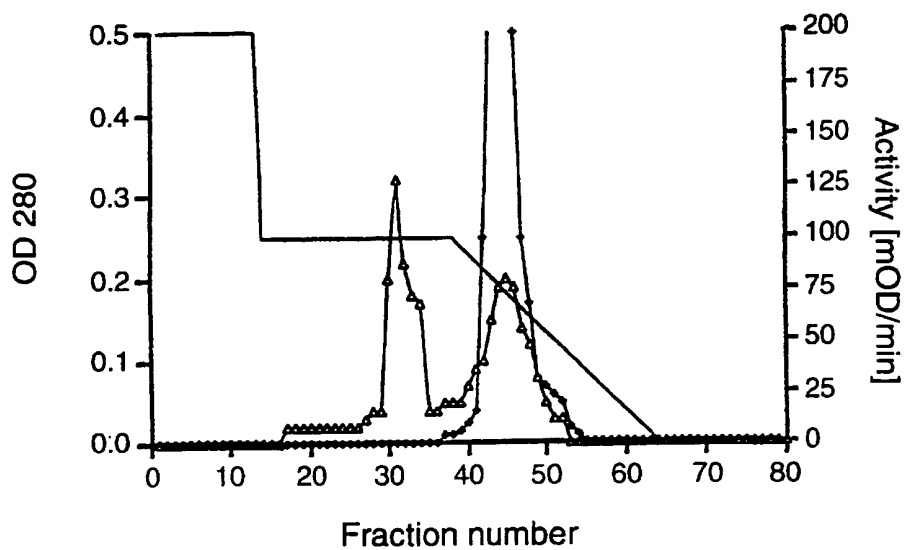


Fig. 1b

2/19

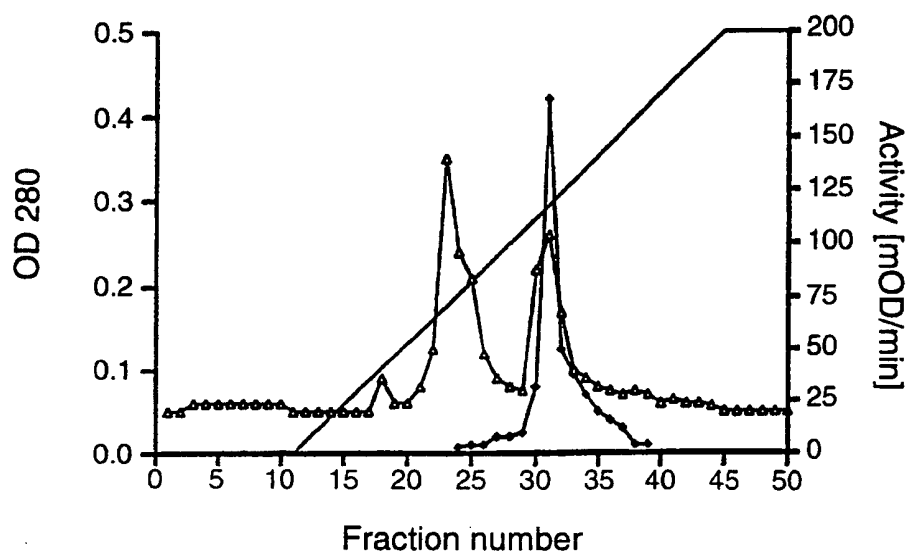


Fig. 1c

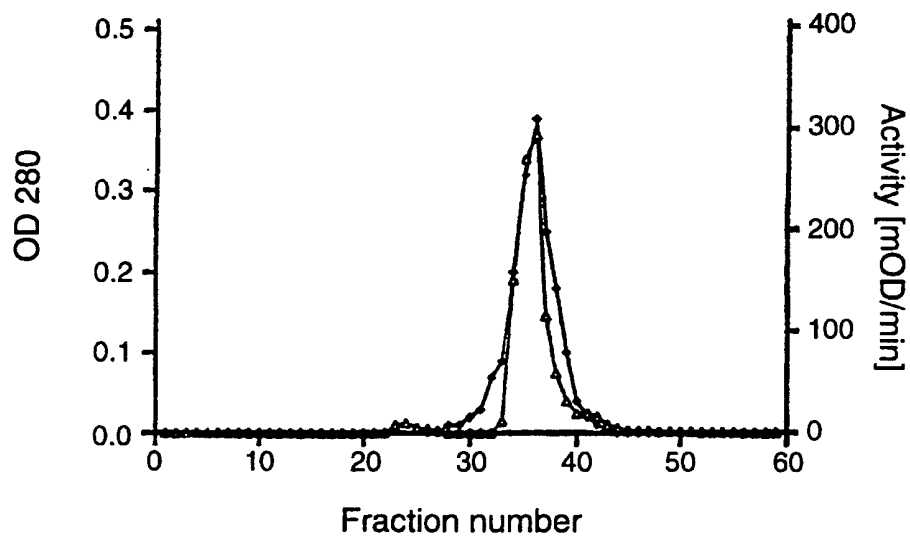


Fig. 1d

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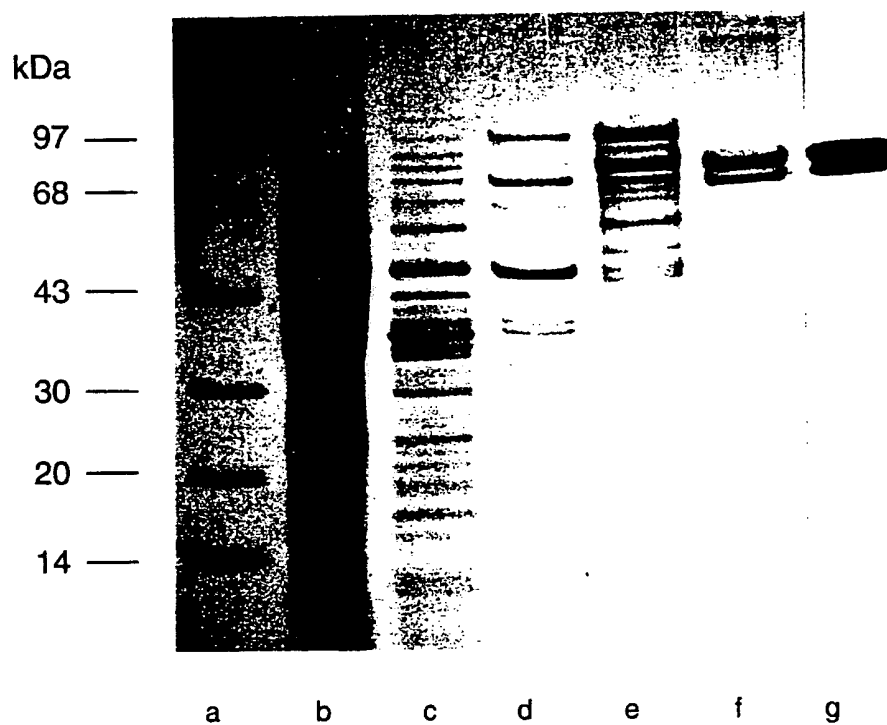


Fig. 2

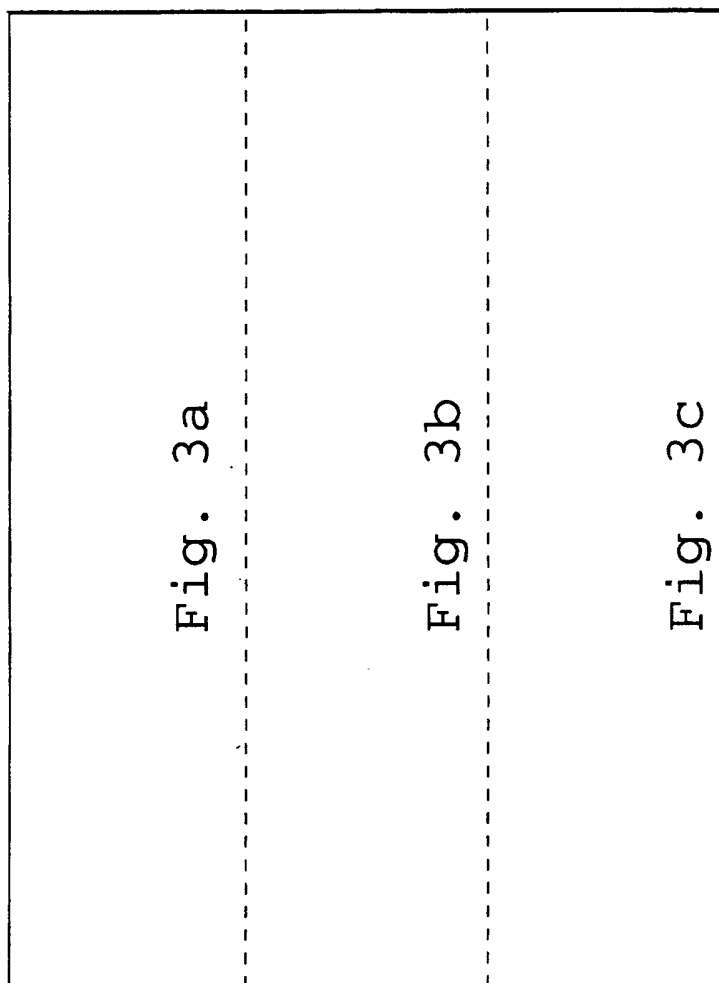


Fig. 3

SEQ ID NO:

26 Mm-FAP 1 MKTWLKITVEGCTTAAALALVLCICVLRPSR-VYKPEGNTK-RALTCLKDILNGTFFSYKTYF
27 Hs-DPP 1 MKTPWRVLLCLIGAAALVTITVPVVLANKGTDIDATDSR-KTYTLLDYLNKNTYRLKLYS
28 Fm-DPP 1 ---MKKKITSLISAVAFHGLSAQEITLDKYSQYRAK-GISGHSASLND-----
29 Pg-DPP 1 -MKRPVITLLIGIVTMCMAQTGNKRPVDLEITSCMFYARSAGSIRSMPD-----
30 PTP-A 1 ---MKKITFQQITFLSVCAITVALPCSAQSPETSCKEETLEQLMPGCKEFYN-FYPEYVV

Mm-FAP 59 PNWISEQEQYTHQS-EDDNTVFYNIETRE--SYIILSNSIMKSVN--ATDYGLISPDQRFV
Hs-DPP 60 LRWISDHEYLYK--QENNILIVENAEYEN--SVFLENSTFDEFGHSINDYSISPDGQFLL
Fm-DPP 48 ---CENYATII--EPTGIANKSYKITSQ--KEKNIIVDGSFQGYT---FSNDESK---IL
Pg-DPP 51 ---CEHYTEMNRERTAITIRNVYASEKAVDITLFSVERARECPFKQIQNIQNYEVSSTGHHEL
56 GLQWMECDNYVFIE---GDDLIVENKANCKSAQITRFSAADLNALMPEGCKEFTIDAFPSFR

Mm-FAP 114 EESDYSKLWRMSYTAITYYINDLQNGEFVRGYELPRPIQYIQMSPVGSKIIAYVYONNIYLYK
Hs-DPP 116 LEYNYVKQWRHSYTAASYDIYDLNKRQLITEERIPNNTQWYIISPVGCHKIAYVWNNIDLYVK
Fm-DPP 92 LQKSSQSIYRHSFELGKFEVVDLKSRTIVSTNNANWIOE-PKFSPDGSKVAFIADNNILFYQ
Pg-DPP 106 LFTDMESIYRHSYRAAVYDIDVRRNLVKPLSEHVGVKVMIPITFSPDGRMVAEVRDNNITFK
113 TLDAGRGILVVLFTQGGVLGCFEDMLARKVITYLFDITNEETASLDFSPVGDVRVAYVRNHNLYIA

Mm-FAP 174 QRP--GPPPFQITVTGRPNRIIFNGIPDWVYEEEMLATKYALMWSPDCKFLAYVEFNDSDI
Hs-DPP 176 IEP--NLPSYRIITWTCKEDITHVNGITIDWVYEEEFVSAYSALMWSENGTELAYAQFNDTEV
Fm-DPP 151 DLN--TGKITQITTDCKKNEIILNGLCDWVYEEEFCHADYYQAN-KAGDALFVVRFDERKV
Pg-DPP 166 KFD--FDTEVQMTDQGINSTINGATDWVYEEEFVNTNLMMS-ADNAELAFVRSDESAN
173 RGGKLGEGMSRAIAVTIDGTETLVYQAVHQHREFGIEKGTFS-PKGSCLAFYRMDQSMV

Mm-FAP 232 PIIAYSYVGGG--QVFRITINIPYKAGAKNPVVRVFIIVDTTYPHMG---PMEVPVPEMI
Hs-DPP 234 PLHEYSFYSDESLOVPEKTVRMPYPKAGAVNPTVKFFVNTDLSSTVNTATSIQITAPASM
Fm-DPP 208 PEINIPITYON--LYPMTYKYPKAGEENSANVAYLYQLSSCKSAQ---LNFGSSEKY
Pg-DPP 223 PEYRMPMYEK--LYFEDYTYKPKAGEKNSTVSLITLVNADRNTKS---VSLPIDADG
232 KPTPIVDYHP---LEAESKPIYVPMAGTPSHHVTVGIVHILATCKTIVY---LQIGEEKEK

Fig. 3a

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Mm-FAP	287	ASSDYFSLTWVSSERVCLQWLKRVQNVSMLSICDFFREDWHAWCPKQEHVBSRTG
Hs-DPP	294	LHGDMYLCVDTWATQERISLQWLRRIQNYSMMDICDYDESSGRWNCCLVARQHHEMSTTG
Fm-DPP	262	YHPLQFQTN--ANDEIVVATNRHONKVDLLKVNTRKTAASV-----K-LFTEEDNAN
Pg-DPP	277	YHPRIAFTD--NADEIVVATNRLONDFKMYVHPKSLVPK-----LILQDMNKRY
	285	FLTNLSNSP--DENILVMAEVNRAONECKNAYDAEIGRFVR-----TLFVEIDKHV
Mm-FAP	347	AGGFVSTPAFSDATSVYKIFSDKDGKHHIHTLKDTVENAIOITSGKWEAIVIFRVTQD
Hs-DPP	354	VGRFRPSEPHFTLDGNSFYKIIISNEEGYRHICYFQIDKRDCTFITKGTWEVIGIEALTSD
Fm-DPP	311	LETNLT-MEFLDDNS--FLWASERDGHRLHYVDAAAGLKKQVSKGDWEIINNYGYNPK
Pg-DPP	326	YDSDWIQTLEKFTTGG--FAYVSEKDGFAHLYLDNKGVMHRRITSGNMDVTKLYGVDS
	335	MEPLHP--LTELPGSNNOFIWQSRDRDGNHLYLYDITGERLIRQVTKGEWEVTFNFAFDPK
Mm-FAP	407	SLFYSSNEFEGYPGRNIVYISIGNSPPSKKCVTCIIRKERCQYVTSFYSKAKKYYALVC
Hs-DPP	414	YLYIISNEYKMGPGGRNLYKIQLSDYTKVT-CLSCENPERCQYYSVSFSKEAKYYQLRC
Fm-DPP	368	-----TKEVYIQTTEKGSINKVSKNINTG---KTQLLSNAEGNNSAFSKTFNFFINTS
Pg-DPP	384	-----GTVFYQSAAESPTRRAVYIDAQR--KTKILSLNVGTN-DALFSGNYAYYINTY
	393	-----GTRLYFESIEASPLERHFYCIDIKGG---KIKDLTPESGMHRTQLSPDGSATIDIF
Mm-FAP	467	Y-GPGIPIISTLHDGRTDQEIQVLEENKELENSELRNIQLPKVETKKLK-DGGLTFMYKMIT
Hs-DPP	473	SGPGIPLVYTLHSSVNDKGLRVLEDSALDKMLQNVOMPSKKLDFHII-LNETKFMVOMIL
Fm-DPP	421	S-TAKVETKYHLKDANGKDVKELONNDDLLNKLKSDNFIAKEFITIPNAGDDQMNAMMIK
Pg-DPP	435	SSAATPANVSVFRSKGAKELRLEEDNVALRERELKAYRYNPKFTTUKTQSSLELNAWIVK
	446	Q-SETVPERKVTVTNIG-KGSHTLLEAKNPDTGYAMPEIRTGTMMAAD--GQTPLYKLTVM
Mm-FAP	525	PPQFDRSKKVPILILQVYGGPCSQSFKSVFAVN---WITYLASKEGIVIALVDGRGTAFQG
Hs-DPP	531	PPHFDKSKKVPILLVYAGPCSQKADIVFRILN---WATYLASTENIIVASFDRGRSGYQG
Fm-DPP	480	PKNEFDPAKKVPVFMFQYSGPGSQQVANSMDGGNGIMFDMLAQKG-VLAVVQVDGRGTGFRG
Pg-DPP	495	PIDFDPSEHVPVLMVQVSCNSQQVLDVYSFD---MEHYLASKG-VVAVCVDRGTGARG
	502	PLHFDPAKKVPVIVVYVGGFHAQLVTKTIRSSVSGGMDIMMAQKG-VAVFTVDSRGCANRG

Fig. 3b

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Mm-FAP	582	DKELHAYVRKLGMEVEDQITAPRKFIEMGFIDEEETAIWGSYGGYVSSIALASGIGLFF
Hs-DPP	588	DKITMHAIRRLCTFEVEDQIEAPQFQSKMGFVNKRRTAIWGSYGGYVTSMTLCSSSGVFF
Fm-DPP	539	TKMKKVTYKKNLCKMEIEDQITPAKMTGNQSYVDKSRIGIFGWSYGGYMASLMTKQADVF
Pg-DPP	551	EEWRKCTYMQLGVFESDDQIAAATAIGQLPYVDAARIGIWGSYGGYTHLMSLCRGNELFF
	561	AAFEQVTHRRILGQTEMAADQMCQGVDFLKQSQNVDAADRIGVHGWSYGGFMHINLMLTHGDFVF
		*
Mm-FAP	642	KCGIAPVSSMEYVASITVSEIFMGLPTKDDNLEPHVKINSTVMARAEYFRNVVDYLLIHGTA
Hs-DPP	648	KCGIAPVSSMEYVESVYTERVMGLPTPEDNLDHYRNSITVMSRAENFKQVENELLIHGTA
Fm-DPP	599	KMGIAVAPVNNRRFYDSIYTERFLQTPQENK--DEYDLNSPTTYAKLLKG-KFELLIHGTA
Pg-DPP	611	KAGIAPVADMPEDYDSVYTERFMRTPKENA--SGYKMSAIDVASQIQG-NLLIVSSSA
	621	KVGAGGGEVILDMNRVEIIMIGERYFDAPQENP--EGYDAANLLKRGDLKG-RLLMIHCAI
		*
Mm-FAP	702	DDNVHFQNSAQIAKALVNAQVDFQAMVYSDQNHGHSGRSQNHLYTHMTHFLKQCFSLSD
Hs-DPP	708	DDNVHFCQSAQISKALVDVGVDFOAMVYIDEDHGHTASSTAHOHTYTHMSHETLKQCFSLP-
Fm-DPP	656	DDNVHFQNSMEFSEALIQNKQDFEMAYEDKNHSHIIGCNTRPQLYEKMTNNIILEN----
Pg-DPP	668	DDNVHLQNTMLETEALVQANIPEDMAIYMDKNHSHIYGCNTRMHLVYTRKAKELFDNL----
	678	DFVVMQHSLELFDACVAKARTYPLYYVYVPSHEENMCPD-BMHLVETIIRYFIDHL----
		*

Fig. 3c

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SEQ ID NO:

PTP-A	556	VDADRI	GVH	GSYGGF	MT	...	RLMLTH	GAID	DPV	WV	QHS	LL	FL	DA	CVK	ARTY	PD	YV	TP	SH	ET	IN	VM	GE	ED	-R	717								
DPP	499	VDAA	RIGI	WGSY	GGYT	TT	...	NLLIV	SGS	AD	DN	HL	QNT	ML	FT	DA	IV	QA	NI	PF	MA	IT	MD	KN	HS	LY	GG	NT	661						
DPP-H1	350	VDP	DR	IAI	YGAS	HGGY	AT	...	PLF	VV	QG	AND	PR	NI	NE	SD	IV	TA	LR	AR	GF	EV	PM	VK	YNE	CH	GF	HR	EN	524					
DPP-H2	640	VNG	KV	CG	QFG	ASYG	GF	MT	...	PL	LL	HG	SV	DT	NP	TA	ES	SN	LY	NA	LL	KI	LG	RE	VE	FT	IE	FT	EQ	DH	FI	LE	PE	RR	810
DPP-H3	495	VDE	DR	IC	AV	CG	ASYG	GF	SV	...	PL	MI	HG	EL	DF	RI	LA	SQ	AA	AF	DA	AA	QL	RG	VP	SE	ML	IV	PD	EN	HW	VL	Q	NA	667

Fig. 4

Influence of Pefablock-serine proteinase inhibitor on *P. gingivalis* growth.

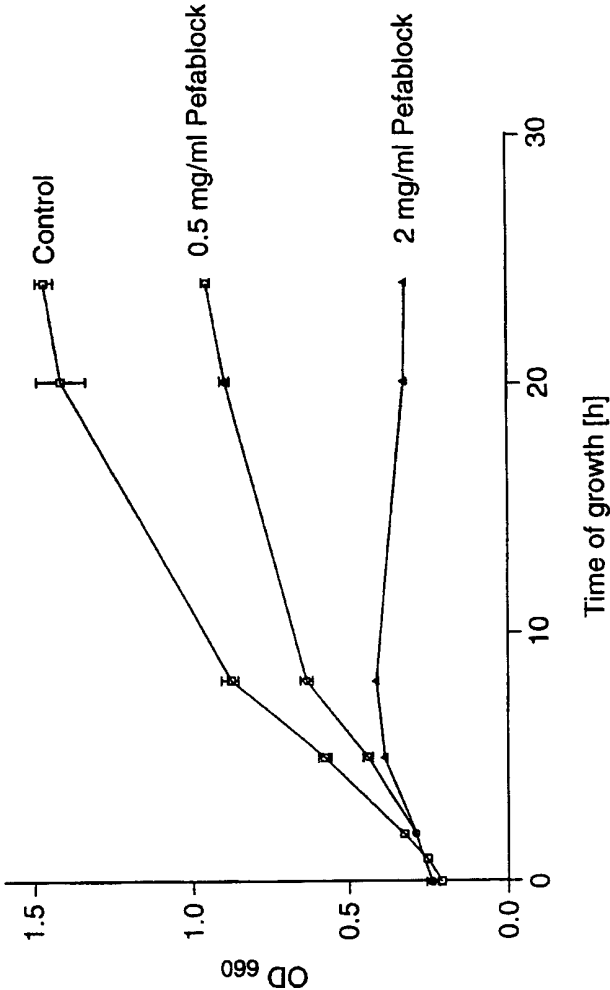


Fig. 5

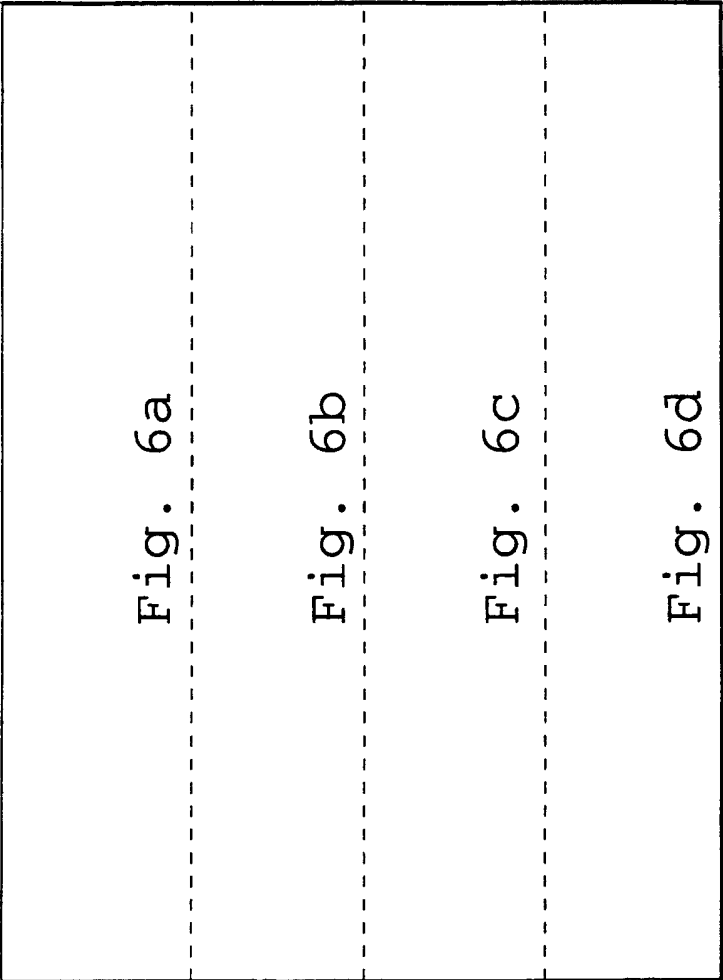


Fig. 6

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SEQ ID NO:
30 126PP 1 MKKIIIFQQLF---LSVCALTVALPCSAQSPETSGKEFTLEQLMPGCKEF--YNFYPEYV
42 87PP 1 ---MPDGEHY--TEMNERT
43 65PP 1 ---MDKGG--NENYHLFA
44 101PP 1 MKKSLMLLTLAATLSSIEAQTIQOMKAGGPWPVRAAFKTDVTGMNGSKYNPADLLRQAY
45 9PP 1 MNKKIIFSMVAAS--IGSAAMTPSAGTNTGHELTPELFMTLSRVSEMAALS--PDGKTAVY

126PP 55 VGLQWMGDNYVF---IEGDDLVFNKANG-----KSAQTTRFSAAQLNALMPEGCKFQ
87PP 16 AIIIRY---NYAS---GKAVDTLFSVER-----ARECPFKQIQ--N-----YE
65PP 14 SNIDG---S---NTRDLTPFDGVK---ASILNMLKEQK--D-----YM
101PP 61 DATDKDLRNVSAADKDGRIAGRKAGSKAERSEMAVYSFALTAEHFAKADIEVFQGRMSLW
9PP 57 AVSFP--DVKII---NKATRELFITVNLD-----GSGRKQITDTESEN-----EYAPAW

126PP 104 TIDAFPSFRITLDAGRC--LVVLFTQGLVGFDMARKVTYL--FDTNEETASLDFSP---
87PP 50 VSSTGFIHLLFTDMES--IYRHSYRAAVDYDVARNLVKPL--SEHVCKVMIPFSE---
65PP 46 IISMNK-----NIPQ---PEPYKLVNVTGEILTQLYEN---KDAANPIQGYEEDK---
101PP 121 LDDKOIGTADSPNSKGDITLRFSSASLSLVPETHLLIKKSIHLEGGTTATDVRVVLNPKTA
9PP 98 MADGKR--IAFMSNEGG---SMQLWVNNADGTERRQLSN-----IEGGLTGFLFSE---

126PP 157 -V-----G-DRAVAVFNHN-LVITARG--GKLGEGMSRAIAMIIDGTETILVYQA--
87PP 103 -P-----C-RMFAFVRDNN-IFIK-----KFDFDTE--VQVHIDGQINSILNGATD
65PP 90 -D-----C-ELRGYSR-----LVNCHIESELVYKD--
101PP 181 RDSSALYPNYTCKERLSLKHMMSGTFLSGGSLSPYTKGYVLTSYRVSNDKNKPAVTYNQLRD
9PP 144 -D-----E-KQVLETKD-----IKFGKRTKDTLVPDLDDK

```

Fig. 6a

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126PP 201 -VHQRERGIEKG--TFWSPKGSCLAFYRM-----DQS-MVKPTPIVDYH---PL
87PP 144 WYEEEPGVTNL--MSWSADNAFLAFVRS-----DES-AVPEYRMPMYED--KL
65PP 112 -LATGEFRRLKK--THWDDTFGVIAENYA-----SKN-KDEAYVLINLD--S
101PP 241 AKGNILLNNEKEALGMPHEDMLMVFKEGNAKRLVAFDPMGKGEKTLVSNLPESQFRM
9PP 170 ATGRIITDLMYK--HMDWEVETIHPPI-----AN-ATDGMITIGKD--H

126PP 243 EAEKPLLYVPMAGT---PSHHMTVGYIYHLA---TG-KTVYLOTGEPKEKFLTNLSWSPDE
87PP 188 YPEDYTKYPKAGE---KNSTVSLHLYNVA---DR-NTKSVSLPIDADGYIPRLAETDNA
65PP 153 DK-TRIVLYDLKQN--K--ITREIFANE--DY-DVSGHLS-RK-----
101PP 301 SPDARYMLFYKQEKGPCKDPLFIHLDPDDRQSDWRDRSQIYLLNAESGVYGPITFGYST
9PP 210 ME-GEPEYEAIPMKPW-----S-GIEDFSWSP--DG--QNIAYASRKKTG--

126PP 296 NIIIVVAE--VNRAQNECKVNAEDAETGTFVVRJLFVEITDKHYVEP--LH-P---LITFLP
87PP 241 DELAVMT--LNRLOQDFKM--YVHPKSLVPKLLQDNKRYVDSDWIQ-T---LKKFTT-
65PP 188 -R-----N-YEIDLMA--VEGEKSVVVVSATYKELIKLME-----KEFK--
101PP 361 TYIMDIAPDSKRRALIGTLSTDWTRRPFRFATIMEYVMEETGKADTLITRDPSIDAIQYTPD
9PP 247 -MAYSLS--TN--SDIYIL--YNLASGRTHNISEGMMGYDTYPK-----FSPD

126PP 346 GSNNQFIWQSR--RDGMNHLIYL-----YDITGRLLIRQVTKGEWEVTNFA---C
87PP 292 CGG--FAYVSE-KDCFAHLYL-----VDNKGVMHRRRIISGNWDVTKLV---C
65PP 224 GKE--FSVM--D-----YDD-----
101PP 421 GKH--LIIVMGS-ADAFGNIGLNKSGVTPNSVEKQFFFDLSIRKATATLKNFNPSVSAG
9PP 287 GKS--IAWISMERDGYES-----DLKRLFVADLATGKRTHVNPTFDYNVDMI

```

Fig. 6b

```

126PP 389 -FDPKGIRLYFESTEAASPLERHFVYCIDIKGCKTRDLTP-ESGMHRTQLSPD-GSATIDIF
87PP 333 -VDAAGI-VFYQSAEESPIRRAMVALDAKGRKTK-LSL-NVGTNDALFSGN-YAYYINTY
65PP 235 --DE--I-ILLIAVQSDKLYGYVQFDIR--TK--KFI--LLYD-L
101PP 478 RFDGRKNN-YVYFRAENG-SRQQLYRLDLKLTLEISQITGTEDVVQWFGVAADNGAMWYSGQ
9PP 332 QMAPDSKGHYFLACKEA--ETNLWEHILKTKIRQLTQGHYADFSVRND--VMLAKR

126PP 446 QSPTVERKVMVTNIGKGSHTLLEAKNPDGTGYAMPETRTG-----TMAADGQTPLYKLT
87PP 388 SSAAITPAVVSFRSKGAKELRTLEDNVALRERLKAYRYNPKFTTLKIQSG-LELNAMIV
65PP 269 ----MBQLK-----EED-----MAEMRPI-----KFKSRDG-LTIHGFIT
101PP 536 SANNADRILYRLDGTGKGLVWDLSSAEKLANIIFTPARDWN-----YTAPDG-TVMEGWXY
9PP 387 HSFELEDDLYRVNLKNGAAQAVTAENKVIILDRITPTCEKR--WMKIIDG-GNMLTWV

126PP 501 MELHFDPAKKYPVLVYVGG--PHADLMTKTWRSVGGWDIYMAQCKGYAMFTVDSRGSAN
87PP 447 KFIDEFDSRHYPVLMVQVSG--FNSQMLD--RYSFD-WEHYLASKGYVMACVDGRGTGA
65PP 299 LFKAALEGKKVPILVNPHG--P--QGRD--SWGPNPQLFAERGYATLQVNFRIISGG
101PP 589 LFPQFDFSKKYPMLVYVYGGTSFINRTLEG--HYSLA--MYAAQGYVMYTLNPSGITC
9PP 443 LPPNFDKNKKYPAILLYCQGG--P--QNTVS-QFMSFRWNLRLLMAEQGYIMIAPNRHGVPG

126PP 559 RGAATFEQVIHRRIGQTEVADQMCVVD-FLKSQSWVDADRIGVHMSYGGFMTINMLTHG
87PP 502 RGEEMRKCTYMQLVFESDDQLAAT-AIGQLPVVDAAKIGIMCMSYGGYITLMSLCRGN
65PP 353 YGKEFLRAGFKQLGRKANDDVEDVLR-VAISQGWVDFDRITAYGASFGGYAILMGLVKIP
101PP 643 YGOEYAAARHVNAWGDRTADEIIGATKEFIRTHSFVNGKKVSCFGASYGGFMLOYLOTKT-
9PP 498 FGQRWNEQISGDYGGQNMFDYLTAVD-EMKKEPVVDGDRIGAVGASYGGSVYWLACHHD

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Fig. 6c

126PP 618 DVFKVGVAGGPMI-----MN--RYEIMYGERVFD--POENPEGYD--AANLLK
87PP 561 GTFKAGIAVAEVA-----MR--FYDSVYITERFMRT--PKENASGYK--MSSALD
65PP 412 DLYACGVYVGVSNITYTFDSFPEYMK--PFKEMVKEILMVDLDNPEFAAIAKE-VSPFFQ
101PP 702 DIFAAAVSHAGISSIS-----N-----YMGSGYMGVSTVASTDSYPMNPDIVAGHSPLFR
9PP 557 KRFAAFIHAAGIFNLEMQYATTEEMWFA-NWDIGGPFWEKDN---VVAQRTYA-TSPHKF

126PP 662 RAGDLKGRIMLIHGAIIDPVVVMQHSLLFLDACVKARTYPDYVVPSPSHENVMGPD-RVHIL
87PP 605 VASQLQGNLITVSGSADDNVHLCNTMLFTEALVQANIPFDMAIYMKNHSIYGGNTENIL
65PP 469 ID-KINKPLFVVGANDPRVNINESDQIVTALRARCFEVVMVKYNECHGFHREENSMEI
101PP 755 AD-KIHTPLILLHGSVDITNVPTAESVNLYNALKILGREVEFIEETQDHFILFEFERIRW
9PP 612 VQ-NWDTPTIIMHGEIDFRLLASQAMAAFDAAQLRGVPSMLIYPPDENHNVLQEQNALLF

126PP 721 YETITRYETDHT-----
87PP 665 YTRKAKFLFDNL-----
65PP 528 YRAMLGFFAKHLKK-----
101PP 814 TNSICAWFAFWLQDDPTWNNELYPPVNL
9PP 671 HRIFFGWLDRWLKK-----

Fig. 6d

15/19

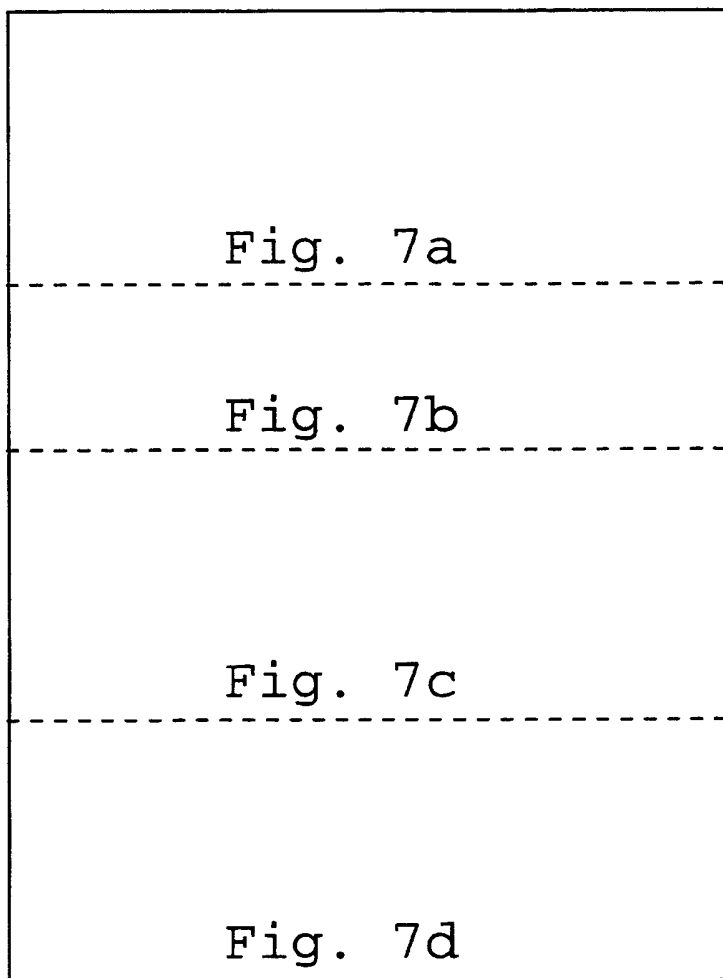


Fig. 7

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P. gingivalis W 83 PTP sequence

SEQ ID NO: 38 13228 atgaagaagacaatcttccaacaactatttctgtctgtttgtgcc
SEQ ID NO: 30 M K K T I F Q Q L F L S V C A
13273 cttacagtggccttgccctgttcggctcagtcctcctgaaacgagt
L T V A L P C S A Q S P E T S
13318 ggtaaggagtttactccttgagcaactgatgcccggaggaaaagag
G K E F T L E Q L M P G G K E
13363 ttttataacttttaccgccgaatacgtgggtcggttgcaatggatg
F Y N F Y P E Y V V G L Q W M
13408 ggagacaattatgtctttatcgaggggtgatgatttagtttttaat
G D N Y V F I E G D D L V F N
13453 aaggcgaatggcaaatcggtcagacgaccagattttctgctgcc
K A N G K S A Q T T R F S A A
13498 gatctcaatgcactcatgccggagggtgcaaatctcagacgact
D L N A L M P E G C K F Q T T
13543 gatgctttcccttcattccgcacactcgatgccggacggggactg
D A F P S F R T L D A G R G L
13588 gtcgttctattttaccaaggaggatttagtcggattcgatatgctt
V V L F T Q G G L V G F D M L
13633 gctcgaaagggtgacttatcttttcgataccaatgaggagacggct
A R K V T Y L F D T N E E T A
13678 tctttggatttttctcctgtgggagaccgtgttgccctatgtcaga
S L D F S P V G D R V A Y V R
13723 aaccataacctttacattgctcgtggaggtaaattgggagaagggt
N H N L Y I A R G G K L G E G
13768 atgtcacgagctatcgctgtgactatcgatggaactgagactctc
M S R A I A V T I D G T E T L
13813 gtatatggccaggccgtacaccagcgtgaattcggtatcgaaaaa
V Y G Q A V H Q R E F G I E K
13858 ggtacattctggtctccaaaaggagctgccttgctttctatcga
G T F W S P K G S C L A F Y R
13903 atggatcagagtatggtgaagcctaccccgatagtggattatcat
M D Q S M V K P T P I V D Y H
13948 ccgctcgaagccgagtcctcaaacgcgtttattaccccatggcagggt
P L E A E S K P L Y Y P M A G
13993 actccgtcacaccacgttacgggttggtatctatcatctggccaca
T P S H H V T V G I Y H L A T
14038 ggtaagaccgtctatctacaaacgggtgaacccaaggaaaaattt
G K T V Y L Q T G E P K E K F
14083 ctgacgaatttgagttggagtcgggacgaaaatatcttgatgta
L T N L S W S P D E N I L Y V
14128 gctgaggtgaatcgtgctcaaacgaatgaaggtaaatagcctat
A E V N R A Q N E C K V N A Y
14173 gacgctgagaccggttagattcgtccgtacgctttttgttgaaacc
D A E T G R F V R T L F V E T
14218 gataaacattatgtagagccgttacatcccctgacattccttcgg
D K H Y V E P L H P L T F L P

Fig. 7a

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14263 ggaagtaacaatcagttcatttggcagagccgctcgcgacggatgg
G S N N Q F I W Q S R R D G W

14308 aaccatctctatctgtatgatactacaggctcgtctgatccgctcag
N H L Y L Y D T T G R L I R Q

14353 gtgacaaaaggggagtgagggttacaaactttgcaggcttcgat
V T K G E W E V T N F A G F D

14398 cccaaggaacacggctctatttcgaaagtaccgaagccagccct
P K G T R L Y F E S T E A S P

14443 ctcgaacgccatttttactgtattgatataaaaggaggaaagaca
L E R H F Y C I D I K G G K T

14488 aaagatctgactccggagtcgggaatgcaccgcactcagctatct
K D L T P E S G M H R T Q L S

14533 cctgatgggttctgccataatcgatatttttcagtcacctactgtc
P D G S A I I D I F Q S P T V

14578 ccgcgtaagggttacagtgacaaatatcggaagggtctcacaca
P R K V T V T N I G K G S H T

14623 ctcttgagggttaagaaccccgatacgggctatgccatgccggag
L L E A K N P D T G Y A M P E

14668 atcagaacgggtaccatcatggcgccgatgggcagacacctctt
I R T G T I M A A D G Q T P L

14713 tattacaagctcacgatgccgcttcatttcgatccggcaaagaaa
Y Y K L T M P L H F D P A K K

14758 tatcctgttattgtctatgtttacggaggacctcatgcccactc
Y P V I V Y V Y G G P H A Q L

14803 gtaaccaagacatggcgcagctctgtcgggtggatgggatattctat
V T K T W R S S V G G W D I Y

14848 atggcacagaaaggctatgccgtctttacggtggtatagtcgcgga
M A Q K G Y A V F T V D S R G

14893 tctgccaatagaggggctgcttttcgagcagggttattcatcgtcgt
S A N R G A A F E Q V I H R R

14938 ttggggcagaccgagatggccgatcagatgtgcgggtgtggatttc
L G Q T E M A D Q M C G V D F

14983 ctcaagagccaatcatgggtggatgccgatagaataggagtacat
L K S Q S W V D A D R I G V H

15028 ggctggagctatgggtggctttatgactacgaatctgatgcttacg
G W S Y G G F M T T N L M L T

15073 cacggcgatgtcttcaaagtcggagtagccggcgggcctgtcata
H G D V F K V G V A G G P V I

15118 gactggaatcgatatgagattatgtacggtgagcggtattttcgat
D W N R Y E I M Y G E R Y F D

15163 gcgccacaggaaaatcccgaaggatac gatgctgccaacctgctc
A P Q E N P E G Y D A A N L L

15208 aaacgagccgggtgatctgaaaggacgacttatgctgattcatgga
K R A G D L K G R L M L I H G

15253 gcgatcgatccggctcgtgggtatggcagcattcactccttttcctt

Fig. 7b

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A I D P V V V W Q H S L L F L
15298 gatgcttgcggtgaaggcacgcacctatcctgactattacgtctat
D A C V K A R T Y P D Y Y V Y
15343 ccgagccacgaacataatgtgatggggccggacagagtacatttg
P S H E H N V M G P D R V H L
15388 tatgaaacaataacccggtatttcacagatcacttatga 15426
Y E T I T R Y F T D H L *

Fig. 7c

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SEQ ID NO:38 ATGAAGAAGACAAATCTTCCAACAACATAATTTCTGTCTGTGTGTGCCCCCTTACAGTGGCCTTGCCCTGTTCTGGC
TCAGTCTCCTGAAACGAGTGGTAAAGAGTTTACTCTTGAGCAACTGATCCCGGAGGAAAGAGTTTATATA
ACTTTTACCCCGAATACGTGGTCGGTTTGC AATGGATGGAGACAAATATATGCTTTTATCGAGGGTGATGAT
TTAGTTTTTAATAAGGCGAATGGCAAAATCGGCTCAGACGACCAGATTTTCTGCTGCCGATCTCAATGCACAT
CATCCGGAGGGATGCAAAATTTACAGACGACTGATGCTTCCCTTCAATTCGGCACACTCGATGCCGGACGGG
GACTGGTCGTTCTATTTACCC AAGAGGATTAGTCGGATTTCGATATGCTTGTGTCGAAAGGTGACTTATCTTT
TTCCGATACCAATGAGGAGACGGCTTCTTTGGATTTTCTCCTGTGGGAGACCGTGTGTCCTATGTCAGAAA
CCATAACCTTTACATTTGCTCGTGGAGGTAATTTGGAGAAAGGTATGTCACGAGCTATCGCTGTGACTATCG
ATGGAACCTGAGACTCTCGTATATGGCCAGGCCGTACACACGCGTGAATTCGGTATCGAAAAAGGTACATTC
TGGTCTCCAAAAGGGAGCTGCCCTTGTCTTCTATCGAATGGATCAGAGTATGGTGAAGCCTACCCCGATAGT
GGATTATCATCCGCTCGAAGCCGAGTCCCAAACCGCTTTATTACCCCATGGCAGGTACTCCGTCACACCCACG
TTACGGTTGGGATCTATCATCTGGCCACAGGTAAGACCGTCTATCTACAAAACGGGTGAACCC AAGGAAAAA
TTTCTGACGAAATTTGAGTTGGAGTCCGGACGAAATATCTTGTATGTAGCTGAGGTGAATCGTGCTCAAAA
CGAATGTAAGGTAATGCCCTATGACGCTGAGACCCGGTAGATTGCTCCGTACGCTTTTGTGTAACCGGATA
AACATTTATGAGAGCCGTTACATCCCTGACATTCCTTCCGGAAAGTAACAATCAGTTCATTTGGCAGAGC
CGTCGGACGGATGGAACCATCTCTATCTGTATGATATACAGTCTGCTGATCCGTCAGGTGACAAAAAGG
GGATGGGAGGTTACAAACTTTTGACGGCTTCGATCCCAAGGGAACACGGCTCTATTTCGAAAAGTACCCGAAG
CCAGCCCTCTCGAACGCCATTTTACTGTATTGATATCAAGGAGGAAAGACAAAAGATCTGACTCCGGAG
TCGGGAATGCACCCGACTCAGCTATCTCCTGTATGTTCTGCCATATTCGATATTTTTCAGTCACTACTGT
CCCGCTAAGGTTACAGTGACAAATATCGGCAAAAGGTCTCACACTCTTGGAGGCTAAGAACCCCGATA
CGGGCTATGCCATGCCGGAGATCAGAACGGGTACCATCATGGCGGCCGATGGGCAGACACCTCTTTATTAC
AAGCTCACGATGCCGCTTCATTTTCGATCCGGCAAAAGAAATATCCTGTTATTGTCTATGTTTACGGAGGACC
TCATGCCCAACTCGTAACCAAGACATGGCGCAGCTCTGTCCGTGGATGGGATATCTATATGGCACAGAAAAG
GCTATGCCGCTCTTACGGTGGATAGTCGGCGGATCTGCCAATAGAGGGGCTGCTTTCGAGCAGGTTATTTCAT
CGTCGTTTGGGGCAGACCGAGATGGCCGATCAGATGTGCGGTGTGGATTTCTCAAGAGCCCAATCATGGGT
GGATGCCGATAGAAATAGGAGTACATGGCTGGAGCTATGGTGGCTTTATGACTACGAATCTGATGCTTACGC
ACGGCGATGTCTTCAAAGTCGGAGTAGCCGGCGGGCTGTCTACAGCTGGAATCGATATGAGATTATGTAC
GGTGACCGTTATTTTCGATGCCCCACAGGAAATCCCGAAGGATACGATGCTGCCAACCTTGCTCAAACGAGC
CGGTGATCTGAAAAGGACGACTTATGCTGATTATCATGGAGCGATCGATCCGGTCTGTGGTATGGCAGCATTCAC
TCCTTTTCTCTGATGCTTGGTGAAGGCACGACCATCTCTGACTATTACGCTCTATCCGAGCCACGAACAT
AATGTGATGGGGCCGACAGAGTACATTTGTATGAACAATAACCCGTTATTTTCACAGATCACTTATGA

Fig. 7d

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/05551

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/57 C12N9/48 A61K39/02

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	KIYAMA, M. ET AL.: "Sequence analysis of the Porphyromonas gingivalis dipeptidyl peptidase IV gene" BIOCHIMICA ET BIOPHYSICA ACTA, vol. 1396, no. 1, 4 March 1998 (1998-03-04), pages 39-46, XP000925951 cited in the application the whole document	7
A	---	1-6, 8-16, 18-20
	-/--	

☒ Further documents are listed in the continuation of box C.☐ Patent family members are listed in annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

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Date of the actual completion of the international search

5 October 2000

Date of mailing of the international search report

10.01.01

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Authorized officer

Fuchs, U

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/05551

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE WPI Section Ch, Derwent Publications Ltd., London, GB; Class B04, AN 1990-053917 XP002149298 & JP 02 005880 A (SUNSTAR KK), 10 January 1990 (1990-01-10)	7
A	abstract	1-6, 8-16, 18-20
P,X	--- BANBULA, A. ET AL.: "Prolyl Tripetidyl Peptidase from Porphyromonas gingivalis" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 274, no. 14, April 1999 (1999-04), pages 9246-9252, XP002149297 the whole document	1-16, 18-20
A	--- KABASHIMA, T. ET AL.: "Cloning, Sequencing, and Expression of the Dipeptidyl Peptidase IV Gene from Flavobacterium meningosepticum in Escherichia coli" ARCHIVES OF BIOCHEMISTRY AND BIOPHYSICS, vol. 320, no. 1, 20 June 1995 (1995-06-20), pages 123-128, XP000925965 the whole document	1-16, 18-20
A	--- KURAMITSU, H.K.: "Proteases of Porphyromonas gingivalis: what don't they do?" ORAL MICROBIOLOGY AND IMMUNOLOGY, vol. 13, no. 5, October 1998 (1998-10), pages 263-270, XP000925947 abstract page 267, column 2, line 34 -page 268, column 1, line 58 -----	1-16, 18-20

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 00/05551

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

Although claims 15 and 16 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-16 AND 18-20 COMPLETELY

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: 1-16 and 18-20 completely

An isolated prolyl tripeptidyl peptidase, active analog, active fragment, or active modification thereof having amidolytic activity for cleavage of a peptide bond present in a target polypeptide having at least 4 amino acids; an isolated prolyl tripeptidyl peptidase, active analog, active fragment, or active modification thereof being isolated from *Porphyromonas gingivalis*; an isolated polypeptide, active analog, active fragment, or active modification thereof having amidolytic activity for cleavage of a peptide bond present in a target polypeptide having at least 4 amino acids; an isolated polypeptide comprising an amino acid sequence having a percentage amino acid identity of greater than 35% with SEQ ID NO: 30; an isolated nucleic acid fragment encoding a prolyl tripeptidyl peptidase, active analog, active fragment, or active modification thereof having amidolytic activity for cleavage of a peptide bond present in a target polypeptide having at least 4 amino acids, an isolated nucleic acid fragment encoding a polypeptide comprising an amino acid sequence having a percentage amino acid identity of greater than 35% with SEQ ID NO: 30; a method of identifying an inhibitor of a prolyl tripeptidyl peptidase, active analog, active fragment, or active modification thereof; a method of reducing growth of a bacterium comprising inhibiting a prolyl tripeptidyl peptidase, active analog, active fragment, or active modification thereof; an immunogenic composition comprising an isolated prolyl tripeptidyl peptidase, or an antigenic analog, antigenic fragment, or antigenic modification thereof, the prolyl tripeptidyl peptidase having amidolytic activity for cleavage of a peptide bond present in a target peptide having at least 4 amino acids; a composition comprising an inhibitor of an isolated prolyl tripeptidyl peptidase;

2. Claim : 17 partially and 21 completely

A method of reducing growth of a bacterium comprising inhibiting a prolyl dipeptidyl peptidase, active analog, active fragment, or active modification thereof; a dipeptidyl peptidase having an amino acid sequence comprising SEQ ID NO: 43;

3. Claim : 17 partially and 22 completely

A method of reducing growth of a bacterium comprising inhibiting a prolyl dipeptidyl peptidase, active analog, active fragment, or active modification thereof; a dipeptidyl peptidase having an amino acid sequence comprising SEQ ID NO: 44;

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

4. Claim : 17 partially and 23 completely

A method of reducing growth of a bacterium comprising inhibiting a prolyl dipeptidyl peptidase, active analog, active fragment, or active modification thereof; a dipeptidyl peptidase having an amino acid sequence comprising SEQ ID NO: 45.

Information on patent family members

PCT/US 00/05551

Form PCT/ISA/210 (patent family annex) (July 1992)

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